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OM protein - protein search, using sw model
Run on: April 8, 2005, 09:58:56 ; Search time 221.333 Seconds
(without alignments)
79.157 Million cell updates/sec

Title: US-09-423-351C-12
Perfect score: 75
Sequence: 1 RGYSTTTAEREIVR 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 6959266 seqs, 116806243 residues
Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :		Pending Patents AA Main:*	
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2:	/cgn2_6/ptodata/1/paa/US06_COMB.pep.*	15	US-09-423-351A-64
3:	/cgn2_6/ptodata/1/paa/US07_COMB.pep.*	97	PCT-US01-00663-26356
4:	/cgn2_6/ptodata/1/paa/US080_COMB.pep.*	75	US-09-864-761-33414
5:	/cgn2_6/ptodata/1/paa/US081_COMB.pep.*	75	US-10-182-993-25553
6:	/cgn2_6/ptodata/1/paa/US082_COMB.pep.*	75	US-10-182-995-19886
7:	/cgn2_6/ptodata/1/paa/US083_COMB.pep.*	75	US-10-182-997-18513
8:	/cgn2_6/ptodata/1/paa/US084_COMB.pep.*	75	US-10-182-998-10177
9:	/cgn2_6/ptodata/1/paa/US085_COMB.pep.*	75	US-10-203-134-26131
10:	/cgn2_6/ptodata/1/paa/US086_COMB.pep.*	75	US-10-203-135-25124
11:	/cgn2_6/ptodata/1/paa/US087_COMB.pep.*	75	US-10-203-136-26119
12:	/cgn2_6/ptodata/1/paa/US088_COMB.pep.*	75	US-10-203-137-26356
13:	/cgn2_6/ptodata/1/paa/US089_COMB.pep.*	75	US-10-203-138-10435
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37:	/cgn2_6/ptodata/1/paa/US60_COMB.pep.*	75	US-10-203-139-25253

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	15	18	US-09-423-351A-12
2	75	100.0	15	18	US-09-423-351A-64
3	75	100.0	97	1	PCT-US01-00663-26356
4	75	100.0	97	23	US-09-864-761-33414
5	75	100.0	97	27	US-10-182-993-25553
6	75	100.0	97	27	US-10-182-995-19886
7	75	100.0	97	27	US-10-182-997-18513
8	75	100.0	97	27	US-10-182-998-10177
9	75	100.0	97	28	US-10-203-134-26131
10	75	100.0	97	28	US-10-203-135-25124
11	75	100.0	97	28	US-10-203-136-26119
12	75	100.0	97	28	US-10-203-137-26356
13	75	100.0	97	28	US-10-203-138-10435
14	75	100.0	97	28	US-10-203-138A-10435
15	75	100.0	97	28	US-10-203-139-25253
16	75	100.0	97	37	US-60-236-359-14763
17	75	100.0	101	22	US-09-791-537-74428
18	75	100.0	104	22	US-09-791-537-74589
19	75	100.0	118	33	US-10-767-795-78974
20	75	100.0	132	37	US-60-565-632-12178
21	75	100.0	132	37	US-60-579-062-12178
22	75	100.0	136	22	US-09-791-537-146472
23	75	100.0	152	22	US-09-791-537-3796
24	75	100.0	153	1	PCT-US01-08631-45856
25	75	100.0	164	19	US-09-513-996A-45859
26	75	100.0	165	37	US-60-324-109-25735
27	75	100.0	168	1	PCT-US01-18569-4044
28	75	100.0	168	28	US-10-264-049-4044
29	75	100.0	179	30	US-10-437-963-203848
30	75	100.0	180	30	US-10-437-963-169247
31	75	100.0	182	37	US-60-581-351-10244
32	75	100.0	186	19	US-09-513-996A-47783
33	75	100.0	186	19	US-09-513-996A-60251
34	75	100.0	189	28	US-10-219-999-59714
35	75	100.0	190	22	US-09-791-537-146432
36	75	100.0	191	20	US-09-698-213A-7
37	75	100.0	193	37	US-60-581-351-10344
38	75	100.0	194	20	US-09-698-213A-11
39	75	100.0	195	22	US-09-791-537-112716
40	75	100.0	196	26	US-10-099-056-1218
41	75	100.0	197	21	US-09-708-427-77890
42	75	100.0	197	22	US-09-760-443-1140
43	75	100.0	197	22	US-09-760-451-103
44	75	100.0	197	28	US-10-201-255-103
45	75	100.0	197	28	US-10-212-054-1140

ALIGNMENTS

RESULT 1
US-09-423-351A-12
; Sequence 12, Application US/09423351A
; GENERAL INFORMATION:
; APPLICANT: The Institute of Cancer Research: Royal
; Cancer Hospital
; TITLE OF INVENTION: Binding Complexes
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; STREET: 172 Locksley Avenue, Apt #3
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: CA 94122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,351A
; FILING DATE: 10-May-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9710762.7
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liou, Anthony Kian-Fong
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-423-351A-12

Query Match 100.0%; Score 75; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAREIVR 15
Db 1 RGYSFTTTAREIVR 15

RESULT 2
US-09-423-351A-64
; Sequence 64, Application US/09423351A
; GENERAL INFORMATION:
; APPLICANT: The Institute of Cancer Research: Royal
; TITLE OF INVENTION: Binding Complexes
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; STREET: 172 Locksley Avenue, Apt #3
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: CA 94122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,351A
; FILING DATE: 10-May-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9710762.7
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liou, Anthony Kian-Fong
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-423-351A-64

Query Match 100.0%; Score 75; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAREIVR 15
Db 1 RGYSFTTTAREIVR 15

RESULT 3
PCT-US01-00663-26356
; Sequence 26356, Application PC/TUS0100663
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: PCT/US01/00663
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26356
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24
; OTHER INFORMATION: EST HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
PCT-US01-00663-26356

Query Match 100.0%; Score 75; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAREIVR 15
Db 75 RGYSFTTTAREIVR 89

RESULT 4
US-09-864-761-33414
; Sequence 33414, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

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11

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: FEATURE:
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 48
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: FEATURE:
: OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
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: FEATURE:
: OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
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: OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
US-10-182-995-19886

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Query Match      100.0%; Score 75; DB 27; Length 97;
Best Local Similarity 100.0%; Pred. NO. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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Db 75 RGYSF TTTAEREIVR 89

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RESULT 7
US-10-182-997-18513
; Sequence 18513, Application US/10182997
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HELA

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FILE OF INTEREST: PB 0004 WO 10
CURRENT APPLICATION NUMBER: US/10/182,997
CURRENT FILING DATE: 2002-08-02

; PRIORITY FILING DATE: 04 February 2000
 ; PRIORITY FILING DATE: 26 May 2000

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, PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
, PRIOR APPLICATION NUMBER: GB 24263.6
, PRIOR FILING DATE: 03 October 2000 (03.10.00)
, PRIOR APPLICATION NUMBER: US 60/236,359
, PRIOR FILING DATE: 27 September 2000 (27.09.00)
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 21 September 2000 (21.09.00)
, PRIOR APPLICATION NUMBER: US 09/608,408
, PRIOR FILING DATE: 30 June 2000 (30.06.00)
, NUMBER OF SEQ ID NOS: 26941
, SOFTWARE: Molecular Dynamics Listing Engine
, SEQ ID NO 18513
, LENGTH: 97

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LENGTH: 57
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

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; OTHER INFORMATION: MAP TO A
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; FEATURE:
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; OTHER INFORMATION: EXPRESSED
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; FEATURE:

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; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUAE 4.00e-51
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; OTHER INFORMATION: EST HUMAN HIT: BE256272.1, EVALUAE 4.00e-50
US-10-182-997-18513

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Query Match      100.0%; Score 75; DB 27; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RGYSFTTTAEREIVR 15
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Db 75 RGYSFTTTAEREIVR 89

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RESULT 8
US-10-182-998-10177
; Sequence 10177, Application US/10182998
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HBL 100
; FILE REFERENCE: PB 0004 WO 9
; CURRENT APPLICATION NUMBER: US/10/182,998
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15009
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 10177
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 78
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
; US-10-182-998-10177

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Qy 1 RGYSFTTTAEREIVR 15
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Db 75 RGYSFTTTAEREIVR 89

RESULT 9
US-10-203-134-26131
Sequence 26131, Application US/10203134
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC AC
TIDE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BONE
FILE REFERENCE: PB 0004 WO 6
CURRENT APPLICATION NUMBER: US/10/203,134
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456


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; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38628
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26131
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 81
; OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
US-10-203-134-26131

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Query Match      100.0%; Score 75; DB 28; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RGYSTTTTAREIVR 15
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Db      75 RGYSTTTTAREIVR 89

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RESULT 10
US-10-203-135-25124
; Sequence 25124, Application US/10203135
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 5
; CURRENT APPLICATION NUMBER: US/10/203,135
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37012
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 25124
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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; OTHER INFORMATION: MAP TO AC006483.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 45
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
US-10-203-135-25124

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Query Match      100.0%; Score 75; DB 28; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RGYSTTTTAREIVR 15
      |||||
Db      75 RGYSTTTTAREIVR 89

```

```

RESULT 11
US-10-203-136-26119
; Sequence 26119, Application US/10203136
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 3
; CURRENT APPLICATION NUMBER: US/10/203,136
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38578
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26119
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 28
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
US-10-203-136-26119

```

```

Query Match      100.0%; Score 75; DB 28; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RGYSTTTTAREIVR 15
      |||||
Db      75 RGYSTTTTAREIVR 89

```

US-10-203-137-26356
; Sequence 26356, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 10435
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 85
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
; US-10-203-138-10435
Query Match 100.0%; Score 75; DB 28; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGYSFTTTAEREIVR 15
Db 75 RGYSFTTTAEREIVR 89
RESULT 14
US-10-203-138A-10435
; Sequence 10435, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 10435
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-203-137-26356
; Sequence 26356, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26356
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
; US-10-203-137-26356
Query Match 100.0%; Score 75; DB 28; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGYSFTTTAEREIVR 15
Db 75 RGYSFTTTAEREIVR 89
RESULT 13
US-10-203-138-10435
; Sequence 10435, Application US/10203138
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138
; CURRENT FILING DATE: 2002-08-02
; PRIOR FILING DATE: 04 February 2000 (04.02.00)

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; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 85
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
US-10-203-138A-10435

```

```

Query Match      100.0%; Score 75; DB 28; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RGYSFTTTAEREIVR 15
       |||||
Db      75 RGYSFTTTAEREIVR 89

```

```

RESULT 15
US-10-203-139-25253
; Sequence 25253, Application US/10203139
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Shaaron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 4
; CURRENT APPLICATION NUMBER: US/10/203,139
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37156
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 25253
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 37
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE271730.1, EVALUE 3.00e-50
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUE 4.00e-51
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
US-10-203-139-25253

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```

Query Match      100.0%; Score 75; DB 28; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RGYSFTTTAEREIVR 15
       |||||

```

Db 75 RGYSFTTTAEREIVR 89

Search completed: April 8, 2005, 11:48:38
Job time : 222.333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 10:51:03 ; Search time 9.4 Seconds
(without alignments)
104.595 Million cell updates/sec

Title: US-09-423-351C-12

Perfect score: 75

Sequence: 1 RGYSTTTTAREIVR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 288363 seqs, 65546468 residues

Total number of hits satisfying chosen parameters: 288363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending Patents AA New.*

- 1: /cgn2_6/ptodata/1/paa/US06 NEW COMB.pcp.*
- 2: /cgn2_6/ptodata/1/paa/US06 NEW COMB.pcp.*
- 3: /cgn2_6/ptodata/1/paa/US07 NEW COMB.pcp.*
- 4: /cgn2_6/ptodata/1/paa/US08 NEW COMB.pcp.*
- 5: /cgn2_6/ptodata/1/paa/US09 NEW COMB.pcp.*
- 6: /cgn2_6/ptodata/1/paa/US10 NEW COMB.pcp.*
- 7: /cgn2_6/ptodata/1/paa/US11 NEW COMB.pcp.*
- 8: /cgn2_6/ptodata/1/paa/US60 NEW COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	15	5	US-09-423-351C-12
2	75	100.0	15	5	US-09-423-351C-12
3	75	100.0	143	8	US-60-655-875-160897
4	75	100.0	153	6	US-10-450-763-45856
5	75	100.0	228	8	US-60-655-875-160314
6	75	100.0	231	8	US-60-655-875-161440
7	75	100.0	239	8	US-60-655-875-161538
8	75	100.0	253	8	US-60-651-235-59
9	75	100.0	253	8	US-60-664-582-577
10	75	100.0	372	8	US-60-655-875-152215
11	75	100.0	375	1	PCT-US04-42360-1194
12	75	100.0	375	1	PCT-US05-03880-99
13	75	100.0	375	8	US-60-651-235-55
14	75	100.0	375	8	US-60-651-235-56
15	75	100.0	375	8	US-60-651-235-60
16	75	100.0	375	8	US-60-651-235-62
17	75	100.0	375	8	US-60-664-582-575
18	75	100.0	375	8	US-60-664-582-576
19	75	100.0	376	8	US-60-664-582-572
20	75	100.0	376	8	US-60-664-582-573
21	75	100.0	388	6	US-10-450-763-57230
22	75	100.0	401	6	US-10-450-763-57230
23	75	100.0	416	6	US-10-450-763-39762
24	72	96.0	181	6	US-10-450-763-41800
25	72	96.0	376	8	US-60-651-235-64

26	70	93.3	201	8	US-60-655-875-122921
27	70	93.3	224	8	US-60-655-875-119898
28	70	93.3	237	8	US-60-655-875-122678
29	70	93.3	363	8	US-60-655-875-121257
30	70	93.3	376	6	US-10-923-035-50
31	70	93.3	376	8	US-60-655-875-121231
32	70	93.3	376	8	US-60-655-875-122271
33	70	93.3	377	1	PCT-US04-23166A-646
34	70	93.3	377	1	PCT-US04-23166A-719
35	70	93.3	377	1	PCT-US04-23166A-790
36	70	93.3	381	8	US-60-655-875-123542
37	66	88.0	211	8	US-60-655-875-123378
38	65	86.7	238	8	US-60-655-875-121411
39	65	86.7	421	6	US-10-450-763-51391
40	62	82.7	195	8	US-60-655-875-160289
41	62	82.7	236	8	US-60-655-875-123397
42	59	78.7	541	6	US-10-450-763-572239
43	58	77.3	247	8	US-60-655-875-123388
44	53	70.7	617	6	US-10-450-763-45854
45	53	70.7	676	6	US-10-450-763-45857

ALIGNMENTS

RESULT 1
US-09-423-351C-12
; Sequence 12: Application US/09423351C
; GENERAL INFORMATION:
; APPLICANT: Willison, Keith
; APPLICANT: Hynes, Gillian
; APPLICANT: Liou, Anthony Kian-Fong
; TITLE OF INVENTION: Binding Complexes
; FILE REFERENCE: 0380-P02097US0
; CURRENT APPLICATION NUMBER: US/09/423.351C
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/GB98/01485
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: GB 9710762.7
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-423-351C-12

Query Match 100.0%; Score 75; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSTTTTAREIVR 15
| | | | | | | | | | | | | | |
Db 1 RGYSTTTTAREIVR 15

RESULT 2
US-09-423-351C-64
; Sequence 64: Application US/09423351C
; GENERAL INFORMATION:
; APPLICANT: Willison, Keith
; APPLICANT: Hynes, Gillian
; APPLICANT: Liou, Anthony Kian-Fong
; TITLE OF INVENTION: Binding Complexes
; FILE REFERENCE: 0380-P02097US0
; CURRENT APPLICATION NUMBER: US/09/423.351C
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/GB98/01485
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: GB 9710762.7

```

; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-423-351C-64

Query Match      100.0%; Score 75; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGYSTTTTAREIVR 15
Db      1 RGYSTTTTAREIVR 15
|||||

RESULT 3
US-60-655-875-160897
; Sequence 160897, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 160897
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit_ID=A48449; Match level="QueryCoverage=100
; OTHER INFORMATION: HitCoverage=38%, E-value=9e-73, Identity=96%", Hit description=Ac
; OTHER INFORMATION: 1A - nematode (Onchocerca volvulus)
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Mol. function-structural constituent of cytoskeleton
; OTHER INFORMATION: Cellular component-cytoskeleton; Biological process-reproduction
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_87320; Strand=-; Position=1-
US-60-655-875-160897

Query Match      100.0%; Score 75; DB 8; Length 143;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGYSTTTTAREIVR 15
Db      74 RGYSTTTTAREIVR 88
|||||

RESULT 4
US-10-450-763-45856
; Sequence 45856, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc

```

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; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 45856
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)..(94)
; OTHER INFORMATION: ACTIN SIGNATURE domain identified by eMATRIX, accession
; OTHER INFORMATION: number PR00190G, p-value=1.600e-21, raw score of 12.62
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (6)..(153)
; OTHER INFORMATION: Actin domain identified by PFam, accession name actin, E-
; OTHER INFORMATION: value=2.4e-98, PFam score of 324.0
US-10-450-763-45856

Query Match      100.0%; Score 75; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGYSTTTTAREIVR 15
Db      37 RGYSTTTTAREIVR 51
|||||

RESULT 5
US-60-655-875-160314
; Sequence 160314, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 160314
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit_ID=XP_311177.1; Match level="QueryCoverage=
; OTHER INFORMATION: =98%, HitCoverage=55%, E-value=1e-128, Identity=99%", Hit descrip
; OTHER INFORMATION: ENSANGP0000019055 [Anopheles gambiae]
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Biological process-reproduction
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_86737; Strand=-; Position=32
US-60-655-875-160314

Query Match      100.0%; Score 75; DB 8; Length 228;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;

```

```
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGYSFTTTAEREIVR 15
    |||||
Db 201 RGYSFTTTAEREIVR 215

RESULT 6
US-60-655-875-161440
; Sequence 161440, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 161440
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Heterodera glycines
; NAME/KEY: misc feature
; LOCATION: (26)-(26)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; TITLE OF INVENTION: Homolog annotation: Hit_ID=NP_505818.1; Match level="QueryCoverag
; OTHER INFORMATION: =98%, HitCoverage=60%, E-value=1e-123, Identity=98%; Hit descrip
; OTHER INFORMATION: actin (41.8 kD) [Caenorhabditis elegans] emb[CAB04675.1]
; OTHER INFORMATION: Hypothetical protein T04C12.5 [Caenorha
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Mol. function=structural constituent of cytoskele
; OTHER INFORMATION: Cellular component=cytoskeleton; Biological process=reproduction
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdNA: vcdNA=SeqID_87863; Strand=+; Position=3-
US-60-655-875-161440
Query Match 100.0%; Score 75; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGYSFTTTAEREIVR 15
    |||||
Db 95 RGYSFTTTAEREIVR 109

RESULT 7
US-60-655-875-161538
; Sequence 161538, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
```

```
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 161538
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Heterodera glycines
; NAME/KEY: misc feature
; LOCATION: (110)-(110)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit_ID=NP_505818.1; Match level="QueryCoverag
; OTHER INFORMATION: =99%, HitCoverage=63%, E-value=1e-130, Identity=98%; Hit descrip
; OTHER INFORMATION: actin (41.8 kD) [Caenorhabditis elegans] emb[CAB04675.1]
; OTHER INFORMATION: Hypothetical protein T04C12.5 [Caenorha
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Mol. function=structural constituent of cytoskele
; OTHER INFORMATION: Cellular component=cytoskeleton; Biological process=reproduction
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdNA: vcdNA=SeqID_87961; Strand=+; Positions=2-
US-60-655-875-161538
Query Match 100.0%; Score 75; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGYSFTTTAEREIVR 15
    |||||
Db 60 RGYSFTTTAEREIVR 74

RESULT 8
US-60-651-235-59
; Sequence 59, Application US/60651235
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001581
; CURRENT APPLICATION NUMBER: US/60/651,235
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 3512
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-651-235-59
Query Match 100.0%; Score 75; DB 8; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGYSFTTTAEREIVR 15
    |||||
Db 74 RGYSFTTTAEREIVR 88

RESULT 9
US-60-664-582-577
; Sequence 577, Application US/60664582
; GENERAL INFORMATION:
; APPLICANT: KIM, Yeounjin et al.
; TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001590
; CURRENT APPLICATION NUMBER: US/60/664,582
; CURRENT FILING DATE: 2005-03-24
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 577
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-60-664-582-577
Query Match      100.0%; Score 75; DB 8; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEREIVR 15
   |||||
Db 74 RGYSTTTTAAEREIVR 88

RESULT 10
US-60-655-875-152215
; Sequence 152215, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 152215
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=seqid 78638; Strand=+; Position=1
; OTHER INFORMATION: -152,435-685,737-1104,1547-1771,2218-2340
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=NP_505818.1; Match level="QueryCoverage=88%, HitCoverage=78%, E-value=1e-161, Identity=88%"; Hit description: actin (41.8 kD) (act-2) [Caenorhabditis elegans] emb[CAB04675.1]
; OTHER INFORMATION: Hypothetical protein T04C12.5 [Caenorhabditis elegans]
US-60-655-875-152215
Query Match      100.0%; Score 75; DB 8; Length 372;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEREIVR 15
   |||||
Db 173 RGYSTTTTAAEREIVR 187

RESULT 11
PCT-US04-42360-1194
; Sequence 1194, Application PC/TUS0442360
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General Hospital
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; PRIOR FILING DATE: 19-Dec-2003
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script
; SEQ ID NO 1194
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
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```
; DATABASE ACCESSION NUMBER: Refseq / NP_112406
; DATABASE ENTRY DATE: 2003-10-05
PCT-US04-42360-1194
Query Match      100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEREIVR 15
   |||||
Db 196 RGYSTTTTAAEREIVR 210

RESULT 12
PCT-US05-03880-99
; Sequence 99, Application PC/TUS0503880
; GENERAL INFORMATION:
; APPLICANT: INANA, GEORGE
; APPLICANT: MCLAREN, MARGARET
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING RETINAL DISEASES
; FILE REFERENCE: 39532-192229
; CURRENT APPLICATION NUMBER: PCT/US05/03880
; CURRENT FILING DATE: 2005-02-09
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 99
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US05-03880-99
Query Match      100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEREIVR 15
   |||||
Db 196 RGYSTTTTAAEREIVR 210

RESULT 13
US-60-651-235-55
; Sequence 55, Application US/60651235
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001581
; CURRENT APPLICATION NUMBER: US/60/651,235
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 3512
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-651-235-55
Query Match      100.0%; Score 75; DB 8; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEREIVR 15
   |||||
Db 196 RGYSTTTTAAEREIVR 210

RESULT 14
US-60-651-235-56
; Sequence 56, Application US/60651235
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
```



```

; FILE REFERENCE: CL001581
; CURRENT APPLICATION NUMBER: US/60/651,235
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 3512
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-651-235-56

Query Match      100.0%; Score 75; DB 8; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGYSTTTTAAEREIVR 15
Db      196 RGYSTTTTAAEREIVR 210

RESULT 15
US-60-651-235-60
; Sequence 60, Application US/60651235
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001581
; CURRENT APPLICATION NUMBER: US/60/651,235
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 3512
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-651-235-60

Query Match      100.0%; Score 75; DB 8; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGYSTTTTAAEREIVR 15
Db      196 RGYSTTTTAAEREIVR 210

Search completed: April 8, 2005, 12:40:14
Job time : 9.4 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-15

Perfect score: 83

Sequence: 1 APPERKYSVWIGGSI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	54	2	I46468
2	83	100.0	67	2	I46473
3	83	100.0	100	2	S14851
4	83	100.0	125	2	A26337
5	83	100.0	137	2	A28258
6	83	100.0	155	2	A60945
7	83	100.0	161	2	S26039
8	83	100.0	204	2	S35256
9	83	100.0	213	2	A61043
10	83	100.0	232	2	I46679
11	83	100.0	308	2	A03000
12	83	100.0	325	2	JC2008
13	83	100.0	327	2	S11452
14	83	100.0	331	2	S24409
15	83	100.0	336	2	T04085
16	83	100.0	349	2	B25819
17	83	100.0	361	2	S68089
18	83	100.0	362	2	A26559
19	83	100.0	362	2	S68090
20	83	100.0	365	2	S49007
21	83	100.0	365	2	A37431
22	83	100.0	370	2	A29664
23	83	100.0	374	1	ATBOB
24	83	100.0	374	1	ATBOG
25	83	100.0	374	2	JC5818
26	83	100.0	375	1	ATBOSM
27	83	100.0	375	1	ATRB
28	83	100.0	375	1	ATRTC
29	83	100.0	375	1	A48324

actin - Acanthamoeba
actin - yeast (Sac)
actin beta - chick
actin - elime mold
actin beta - human
actin gamma 1 - hu
actin gamma - mouse
actin gamma - mous
actin beta, non-mu
actin - yeast (Sac)
actin gamma, cytos
actin, cytosolic (
actin gamma - Emer
actin 1 - Pneumocy
hypothetical prote
actin - yeast (Klu

ALIGNMENTS

RESULT 1

I46468

actin - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C:Accession: I46468

R:Bacich, D.J.; Rohan, R.M.; Norman, R.J.; Rodgers, R.J.

Endocrinology 135, 735-744, 1994

A>Title: Characterization and relative abundance of alternatively spliced luteinizing ho

A:Reference number: I46466; MUID:94307184; PMID:7519389

A:Accession: I46468

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-54 <BAC>

A:Cross-references: UNIPROT:Q28539; EMBL:U08283; NID:g475579; PIDN:AAA20649.1; PID:g4755

C:Superfamily: actin

Query Match 100.0%; Score 83; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGGSI 15

Db 30 APPERKYSVWIGGSI 44

RESULT 2

I46473

alpha-actin - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C:Accession: I46473

R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.

Nature 302, 718-721, 1983

A>Title: A new tropomyosin T and cDNA clones for 13 different muscle proteins, found by sho

A:Reference number: I46471; MUID:83167564; PMID:6687628

A:Accession: I46473

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-67 <PUT>

A:Cross-references: UNIPROT:P02568; EMBL:V00874; NID:g1432; PIDN:CAA24243.1; PID:g833791

C:Superfamily: actin

Query Match 100.0%; Score 83; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGGSI 15

Db 23 APPERKYSVWIGGSI 37

Fri Apr 8 14:14:23 2005

```
RESULT 3
SI4851
actin - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: SI4851
R:Burn, T.C.; Tobin, S.L.
submitted to the EMBL Data Library, October 1990
A:Reference number: SI4851
A:Accession: SI4851
A:Molecule type: DNA
A:Residues: 1-100 <BUR>
A:CROSS-references: UNIPROT:P02572; EMBL:X54848; NID:G7549; PIDN:CAA38618.1; PID:G7550
C:Genetics:
A:Gene: FlyBase:Act42A
A:CROSS-references: FlyBase:FBgn0000043
C:Superfamily: actin
C:Keywords: cell motility; cytoskeleton; microfilament; mitosis; structural protein

Query Match 100.0%; Score 83; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGGSI 15
|||||
Db 56 APPERKYSVWIGGSI 70

RESULT 4
A26337
actin, skeletal muscle - Iberian ribbed newt (fragment)
C:Species: Pleurodeles waltlii (Iberian ribbed newt)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A26337
R:Khrestchatsky, M.; Pontes, M.
J. Mol. Biol. 193, 409-412, 1987
A:Title: There is an alpha-actin skeletal muscle-specific gene in a salamander (Pleurodeles waltlii)
A:Reference number: A26337; MUID:87254218; PMID:3453122
A:Accession: A26337
A:Molecule type: DNA
A:Residues: 1-135 <KHR>
A:CROSS-references: UNIPROT:P10994; GB:X05106; NID:G64248; PIDN:CAA28753.1; PID:G64249
C:Superfamily: actin
C:Keywords: muscle; skeletal muscle

Query Match 100.0%; Score 83; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGGSI 15
|||||
Db 81 APPERKYSVWIGGSI 95

RESULT 5
A28258
actin 5C - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
R:Vigoreaux, J.O.; Tobin, S.L.
Genes Dev. 1, 1161-1171, 1987
A:Title: Stage-specific selection of alternative transcriptional initiation sites from the 5' end of the actin 5C gene
A:Reference number: A28258; MUID:88112795; PMID:3123314
A:Accession: A28258
A:Molecule type: mRNA
A:Residues: 1-137 <VIG>
A:CROSS-references: UNIPROT:P10987
A:Note: the authors translated the codon GAG for residue 96 as Gly
C:Genetics:
A:Gene: FlyBase:Act5C
A:CROSS-references: FlyBase:FBgn0000042
C:Superfamily: actin
```

```
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 83; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGGSI 15
|||||
Db 93 APPERKYSVWIGGSI 107

RESULT 6
A60945
actin homolog FAR, testicular - starfish (Pisaster ochraceus) (fragments)
C:Species: Pisaster ochraceus
C>Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A60945
R:Boom, J.D.G.; Smith, M.J.
J. Exp. Zool. 250, 312-320, 1989
A:Title: Molecular analyses of gene expression during sea star spermatogenesis.
A:Reference number: A60945; MUID:89341860; PMID:2474626
A:Accession: A60945
A:Molecule type: mRNA
A:Residues: 1-155 <BOO>
A:CROSS-references: UNIPROT:O7M3Y6
A:Note: authors translated the codon TTG for residue 77 as Ile, and TGC for residue 81 a
C:Superfamily: actin

Query Match 100.0%; Score 83; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGGSI 15
|||||
Db 134 APPERKYSVWIGGSI 148

RESULT 7
S26039
actin - shore pine (fragment)
C:Species: Pinus contorta (shore pine)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S26039
R:Kenny, J.R.; Dancik, B.P.; Florence, L.Z.; Nargang, F.B.
Can. J. For. Res. 18, 1595-1602, 1988
A:Title: Nucleotide sequence of the carboxy-terminal portion of a lodgepole pine actin g
A:Reference number: S26039
A:Accession: S26039
A:Molecule type: DNA
A:Residues: 1-161 <KEN>
A:CROSS-references: UNIPROT:P24902; EMBL:M36171; NID:G169373; PIDN:AAA33775.1; PID:G1693
C:Genetics:
A:Introns: 140/3
C:Superfamily: actin

Query Match 100.0%; Score 83; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGGSI 15
|||||
Db 117 APPERKYSVWIGGSI 131

RESULT 8
S35256
actin (clone Tac9) - common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 06-Jun-1997
C:Accession: S35256
R:Thangavelu, M.; Belostotsky, D.; Bevan, M.W.; Flavell, R.B.; Rogers, H.J.; Lonsdale, D.
Mol. Gen. Genet. 240, 290-295, 1993
```

A:Title: Partial Characterization of the Nicotiana tabacum actin gene family: evidence for
A:Reference number: S35256; MUID:93360910; PMID:8355661
A:Accession: S35256
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-204 <THA>
A:Cross-references: EMBL:X69885
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Superfamily: actin

Query Match 100.0%; Score 83; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSI 15
|||||
Db 181 APPERKYSVWIGSI 195

RESULT 9
A61043
actin Cal5 - sea squirt (Styela clava) (fragments)
C:Species: Styela clava
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A61043
R:Beach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A:Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian Sc
A:Reference number: A61043; MUID:90298580; PMID:2361333
A:Accession: A61043
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-213 <BEA>
A:Cross-references: UNIPROT:Q7M3Y7
C:Comment: This sequence is expressed in cells undergoing rapid cell division.
C:Superfamily: actin
C:Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 83; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSI 15
|||||
Db 169 APPERKYSVWIGSI 183

RESULT 10
146679
alpha-smooth muscle actin - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
C:Accession: I46679
R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
A:Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by sh
A:Reference number: I46471; MUID:83167564; PMID:6687628
A:Accession: I46679
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <PUT>
A:Cross-references: GB:J00654; MUID:g164748; PIDN:AAA31154.1; PID:g164750
C:Genetics:
C:Superfamily: actin

Query Match 100.0%; Score 83; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSI 15
|||||

Db 188 APPERKYSVWIGSI 202

RESULT 11
A03000
actin 3 - fruit fly (Drosophila melanogaster) (fragments)
C:Species: Drosophila melanogaster
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A03000
R:Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
A:Title: The actin genes of Drosophila: protein coding regions are highly conserved but
A:Reference number: A03000; MUID:81210174; PMID:6263481
A:Accession: A03000
A:Molecule type: DNA
A:Residues: 1-308 <FYR>
A:Cross-references: UNIPROT:P02572
A:Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
A:Note: the authors translated the codon GTT for residue 263 as Ile
C:Genetics:
A:Gene: FlyBase:Act42A
A:Cross-references: FlyBase:FBgn0000043
A:Map position: 42A
C:Superfamily: actin
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 83; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSI 15
|||||
Db 264 APPERKYSVWIGSI 278

RESULT 12
JC2008
actin homolog protein - red swamp crayfish
C:Species: Procambarus clarkii (red swamp crayfish)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C:Accession: JC2008
R:Kang, W.K.; Naya, Y.
Gene 133, 303-304, 1993
A:Title: Sequence of the cDNA encoding an actin homolog in the crayfish Procambarus clark
A:Reference number: JC2008; MUID:94040829; PMID:8224920
A:Accession: JC2008
A:Molecule type: mRNA
A:Residues: 1-325 <KAN>
A:Cross-references: GB:D14612; NID:g434784; PIDN:BAA03463.1; PID:g434785
A:Experimental source: muscle
C:Superfamily: actin
C:Keywords: muscle contraction

Query Match 100.0%; Score 83; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSI 15
|||||
Db 281 APPERKYSVWIGSI 295

RESULT 13
S11452
actin (clone 302) - brine shrimp (fragment)
C:Species: Artemia sp. (brine shrimp)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S11452
R:Macias, W.T.; Sastre, L.
Nucleic Acids Res. 18, 5219-5225, 1990
A:Title: Molecular cloning and expression of four actin isoforms during Artemia develop
A:Reference number: S11450; MUID:90384823; PMID:2402445

Fri Apr 8 14:14:23 2005

us-09-423-351c-15.rpr

Search completed: April 8, 2005, 10:53:08
Job time : 9.33333 secs

```
A:Accession: S11452
A:Molecule type: mRNA
A:Residues: 1-327 <MAC>
A:Cross-references: UNIPROT:P18602; EMBL:X52604; NID:g5666; PIDN:CAA36837.1; PID:g829162
C:Superfamily: actin
C:Keywords: methylated amino acid; structural protein
F:25/Modified site: 3'-methylhistidine (His) #status predicted

Query Match      100.0%; Score 83; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APPERKYSVWIGGSI 15
Db      283 APPERKYSVWIGGSI 297
|||||

RESULT 14
S24409
actin - brown alga (Costaria costata) (fragment)
C:Species: Costaria costata
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S24409
R:Bhattacharya, D.; Stickel, S.K.; Sogin, M.L.
J. Mol. Evol. 33, 525-536, 1991
A:Title: Molecular phylogenetic analysis of actin genic regions from Achlya bisexualis
A:Reference number: S24408; MUID:92139446; PMID:1779434
A:Accession: S24409
A:Molecule type: mRNA
A:Residues: 1-331 <BHA>
A:Cross-references: UNIPROT:P30161; EMBL:X59937; NID:g17956; PIDN:CAA42560.1; PID:g17957
C:Superfamily: actin
C:Keywords: methylated amino acid
F:29/Modified site: 3'-methylhistidine (His) #status predicted

Query Match      100.0%; Score 83; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APPERKYSVWIGGSI 15
Db      287 APPERKYSVWIGGSI 301
|||||

RESULT 15
T04085
actin - maize (fragment)
C:Species: Zea mays (maize)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04085
R:de Sa, M.; Drouin, G.
Mol. Biol. Evol. 13, 1198-1212, 1996
A:Title: Phylogeny and substitution rates of angiosperm actin genes.
A:Reference number: Z15197; MUID:97051711; PMID:8896372
A:Accession: T04085
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-336 <DES>
A:Cross-references: UNIPROT:P93638; EMBL:U60513; NID:g1498392; PIDN:AAB40107.1; PID:g149
C:Genetics:
A:Gene: Maz63
A:Note: Intron positions not resolved (incomplete sequence)
C:Superfamily: actin
C:Keywords: cytoskeleton; structural protein

Query Match      100.0%; Score 83; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APPERKYSVWIGGSI 15
Db      313 APPERKYSVWIGGSI 327
|||||
```

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-15
Perfect score: 83
Sequence: 1 APPERKYSVWIGSI 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	45	2 Q6J0R3	Q6J0R3 hydra atten
2	83	100.0	45	2 Q6J0R4	Q6J0R4 hydra atten
3	83	100.0	50	2 Q9DDZ2	Q9DDZ2 microterus
4	83	100.0	53	2 Q6S063	Q6S063 picea maria
5	83	100.0	54	2 Q28539	Q28539 oviss aries
6	83	100.0	55	2 Q8AY69	Q8AY69 oncorhynch
7	83	100.0	56	2 Q57575	Q57575 cynops pyrr
8	83	100.0	58	2 Q8WQ49	Q8WQ49 gecarcinus
9	83	100.0	61	2 Q23877	Q23877 dictyosteli
10	83	100.0	65	2 Q23878	Q23878 dictyosteli
11	83	100.0	74	2 Q8GZK2	Q8GZK2 arabidopsis
12	83	100.0	76	2 Q40946	Q40946 ipomoea nil
13	83	100.0	76	2 Q40947	Q40947 ipomoea nil
14	83	100.0	76	2 Q40952	Q40952 ipomoea nil
15	83	100.0	83	2 Q23875	Q23875 dictyosteli
16	83	100.0	86	2 Q8GUQ6	Q8GUQ6 pinus taeda
17	83	100.0	87	2 Q23879	Q23879 dictyosteli
18	83	100.0	88	2 Q23880	Q23880 dictyosteli
19	83	100.0	88	2 Q8GZH0	Q8GZH0 arabidopsis
20	83	100.0	88	2 Q8GZH1	Q8GZH1 arabidopsis
21	83	100.0	88	2 Q8GZH2	Q8GZH2 arabidopsis
22	83	100.0	88	2 Q8GZH3	Q8GZH3 arabidopsis
23	83	100.0	88	2 Q8GZH4	Q8GZH4 arabidopsis
24	83	100.0	88	2 Q8GZH5	Q8GZH5 arabidopsis
25	83	100.0	88	2 Q8GZH6	Q8GZH6 arabidopsis
26	83	100.0	88	2 Q8GZH7	Q8GZH7 arabidopsis
27	83	100.0	88	2 Q8GZH8	Q8GZH8 arabidopsis
28	83	100.0	88	2 Q8GZH9	Q8GZH9 arabidopsis
29	83	100.0	88	2 Q8GZ10	Q8GZ10 arabidopsis
30	83	100.0	88	2 Q8GZ11	Q8GZ11 arabidopsis
31	83	100.0	88	2 Q8GZ12	Q8GZ12 arabidopsis

32	83	100.0	88	2 Q8GZ13	Q8GZ13 arabidopsis
33	83	100.0	88	2 Q8GZ14	Q8GZ14 arabidopsis
34	83	100.0	88	2 Q8GZ15	Q8GZ15 arabidopsis
35	83	100.0	88	2 Q8GZ16	Q8GZ16 arabidopsis
36	83	100.0	88	2 Q8GZ17	Q8GZ17 arabidopsis
37	83	100.0	88	2 Q8GZ18	Q8GZ18 arabidopsis
38	83	100.0	88	2 Q8GZ19	Q8GZ19 arabidopsis
39	83	100.0	88	2 Q8GZJ0	Q8GZJ0 arabidopsis
40	83	100.0	88	2 Q8GZJ1	Q8GZJ1 arabidopsis
41	83	100.0	88	2 Q8GZJ3	Q8GZJ3 arabidopsis
42	83	100.0	88	2 Q8GZJ4	Q8GZJ4 arabidopsis
43	83	100.0	88	2 Q8GZJ5	Q8GZJ5 arabidopsis
44	83	100.0	88	2 Q8GZJ6	Q8GZJ6 arabidopsis
45	83	100.0	88	2 Q8GZJ7	Q8GZJ7 arabidopsis

ALIGNMENTS

RESULT 1
Q6J0R3 PRELIMINARY; PRT; 45 AA.
AC Q6J0R3;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Actin 1.7 (Fragment).
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=201;
RX MEDLINE=90108717; PubMed=2606361; DOI=10.1016/0378-1119(89)90139-X;
RA Fisher D.A., Bode H.R.;
RT "Nucleotide sequence of an actin-encoding gene from Hydra attenuata: structural characteristics and evolutionary implications.";
RL Gene 84:55-64(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=201;
RA Fisher D.A., Bode H.R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY609160; AAT37545.1;
DR GO: GO:0005884; C:actin filament; IEA.
DR GO: GO:0003774; F:motor activity; IEA.
DR GO: GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro: IPR004001; Actin.
DR PROSITE: PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 45 AA; 5159 MW; 7796DEF78D574D0 CRC64;

Query Match 100.0%; Score 83; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
| | | | | | | | | | | | | | | |
DB 1 APPERKYSVWIGSI 15

RESULT 2
Q6J0R4 PRELIMINARY; PRT; 45 AA.
AC Q6J0R4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Actin 1.6 (Fragment).
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Anthomedusae;
OC Hydridae; Hydra.

```

OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=201;
RX MEDLINE=90108717; PubMed=2606361; DOI=10.1016/0378-1119(89)90139-X;
RA Fisher D.A., Bode H.R.;
RT "Nucleotide sequence of an actin-encoding gene from Hydra attenuata: structural characteristics and evolutionary implications.";
RL Gene 84:55-64(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=201;
RA Fisher D.A., Bode H.R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY609159; AAT37544.1; -.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 45 AA; 5159 MW; 7796EDEF78D574D0 CRC64;

Query Match 100.0%; Score 83; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
DB 1 APPERKYSVWIGSI 15

RESULT 3
Q9DDZ2 PRELIMINARY; PRT; 50 AA.
AC Q9DDZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Micropterus salmoides (Largemouth bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Centrarchidae; Micropterus.
OX NCBI_TaxID=27706;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Bowman C.J., Sabo-Attwood T.L., Lee H.S., Denslow N.D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF253319; AAG44624.1; -.
DR HSP; P02568; IMA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 50
SQ SEQUENCE 50 AA; 5694 MW; 44542890573899BB CRC64;

Query Match 100.0%; Score 83; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
DB 20 APPERKYSVWIGSI 34

RESULT 4
Q65063 PRELIMINARY; PRT; 53 AA.
ID Q65063

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AC Q65063;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=Sb31;
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98278823; PubMed=9611216;
RA Perry D.J., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes. Development, characterization and analysis of linkage in black spruce.";
RL Genetics 149:1089-1098(1998).
DR EMBL; AF051224; AAC32125.1; -.
DR HSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 53 AA; 5959 MW; 024C6B530AB1CF4E CRC64;

Query Match 100.0%; Score 83; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
DB 9 APPERKYSVWIGSI 23

RESULT 5
Q28539 PRELIMINARY; PRT; 54 AA.
ID Q28539
AC Q28539;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpora lutea;
RX MEDLINE=94307184; PubMed=7518389; DOI=10.1210/en.135.2.735;
RA Bacich D.J., Rohan R.M., Norman R.J., Rodgers R.J.;
RT "Characterization and relative abundance of alternatively spliced luteinizing hormone receptor messenger ribonucleic acid in the ovine ovary.";
RL Endocrinology 135:735-744(1994).
DR EMBL; U08283; AAA20649.1; -.
DR PIR; I46468; I46468.
DR HSP; P02568; IMA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 54
SQ SEQUENCE 54 AA; 5963 MW; 8AFDEAC1DCC70AD CRC64;

Query Match 100.0%; Score 83; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;

```


Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGGSI 15

Db 30 APPERKYSWIGGSI 44

RESULT 6

Q8AY69 PRELIMINARY; PRT; 55 AA.

AC Q8AY69; (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Beta-actin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neoplatygerii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Schwindt A.R., Alonso M., Leong J.C., Schreck C.B.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF50583; AAN74801.1; -;
DR HSSP; P02568; 1MA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6163 MW; 9A4319FB34DD79D8 CRC64;

Query Match 100.0%; Score 83; DB 2; Length 55;

Best Local Similarity 100.0%; Pred. No. 9.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGGSI 15

Db 25 APPERKYSWIGGSI 39

RESULT 7

OS7575 PRELIMINARY; PRT; 56 AA.

AC OS7575;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha cardiac actin (Fragment).
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.;
RT "pax-6 gene expression in newt eye development.";
RL Dev. Genes Evol. 207:167-176(1997).
DR EMBL; D64017; BAA24031.1; -;
DR HSSP; P02568; 1LCU.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
FT NON_TER 56
SQ SEQUENCE 56 AA; 6339 MW; 3532A4205AC50B5 CRC64;

Query Match 100.0%; Score 83; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 9.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGGSI 15

Db 12 APPERKYSWIGGSI 26

RESULT 8

Q8WQ49 PRELIMINARY; PRT; 58 AA.

AC Q8WQ49;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta-actin (Fragment).
GN Name=act2;
OS Gecarcinus lateralis (Blackback land crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Grapsoidea; Gecarcinidae; Gecarcinus.
OX NCBI_TaxID=6769;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257216;
RA Varadraj K., Kumari S.S., Skinner D.M.;
RT "Actin-encoding cDNAs and gene expression during the intermolt cycle
of the Bermuda land crab Gecarcinus lateralis.";
RL Gene 171:177-184(1996).
DR EMBL; L76530; AAL40078.1; -;
DR HSSP; P02568; 1KXP.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6467 MW; AAE2E1F022262659 CRC64;

Query Match 100.0%; Score 83; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGGSI 15

Db 14 APPERKYSWIGGSI 28

RESULT 9

Q23877 PRELIMINARY; PRT; 61 AA.

AC Q23877;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Actin 5 (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3;
RX MEDLINE=80101584; PubMed=293714;
RA Firtel R.A., Timm R., Kimmel A.R., McKeown M.;
RT "Unusual nucleotide sequences at the 5' end of actin genes in
Dictyostelium discoideum.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:6206-6210(1979).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3;
RX MEDLINE=82122583; PubMed=6276562;
RA McKeown M., Firtel R.A.;

Fri Apr 8 14:14:23 2005

us-09-423-351c-15.rup

RT "Evidence for sub-families of actin genes in Dictyostelium as
 RT determined by comparisons of 3' end sequences.";
 RL J. Mol. Biol. 151:593-606(1981).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3;
 RX MEDLINE=82260445; PubMed=6286214;
 RA McKeown M., Firtel R.A.;
 RT "Actin multigene family of Dictyostelium.";
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
 DR EMBL; K02958; AAA33152.1; -;
 DR HSSP; P02577; 1NM1.
 DR DictyBase; DB0220447; act5.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 SQ SEQUENCE 61 AA; 6826 MW; 7DB7AAA3408659FA CRC64;

Query Match 100.0%; Score 83; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
 DB 17 APPERKYSVWIGSI 31

RESULT 10

Q23878 ID Q23878 PRELIMINARY; PRT; 65 AA.
 AC Q23878;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Slime mold (D. discoideum) actin 6 (fragment).
 OC Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234564; PubMed=6894715; DOI=10.1016/0092-8674(81)90105-7;
 RA McKeown M., Firtel R.A.;
 RT "Differential expression and 5' end mapping of actin genes in
 Dictyostelium.";
 RL Cell 24:799-807(1981).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=82122583; PubMed=6276562;
 RA McKeown M., Firtel R.A.;
 RT "Evidence for sub-families of actin genes in Dictyostelium as
 determined by comparisons of 3' end sequences.";
 RL J. Mol. Biol. 151:593-606(1981).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=82260445; PubMed=6286214;
 RA McKeown M., Firtel R.A.;
 RT "Actin multigene family of Dictyostelium.";
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
 DR EMBL; K02959; AAA33154.1; -;
 DR HSSP; P02577; 1NM1.
 DR DictyBase; DB0185126; act6.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 SQ SEQUENCE 65 AA; 7243 MW; 1B2FB441FA085AF0 CRC64;

Query Match 100.0%; Score 83; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
 DB 21 APPERKYSVWIGSI 35

RESULT 11

Q8GZK2 ID Q8GZK2 PRELIMINARY; PRT; 74 AA.
 AC Q8GZK2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Actin 8 (fragment).
 OC Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22453515; PubMed=12566397; DOI=10.1101/gr.593403;
 RA Hall S.E., Kettler G., Preuss D.;
 RT "Centromere satellites from Arabidopsis populations: maintenance of
 conserved and variable domains.";
 RL Genome Res. 13:195-205(2003).
 DR EMBL; AF494804; AAN77977.1; -;
 DR HSSP; P02577; 1NM1.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 SQ SEQUENCE 74 AA; 8010 MW; 39552CEF499C080F CRC64;

Query Match 100.0%; Score 83; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
 DB 51 APPERKYSVWIGSI 65

RESULT 12

Q40946 ID Q40946 PRELIMINARY; PRT; 76 AA.
 AC Q40946;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Actin (fragment).
 GN Name=pharbitis nil actin 3-3;
 OS Ipomoea nil (Japanese morning glory) (Pharbitis nil).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Convolvulaceae; Ipomoeaceae; Ipomoea.
 OX NCBI_TaxID=35883;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Violet; TISSUE=apical meristem;
 RA Sage-Ono K., Ono M., Kamada H.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D78206; BAA11309.1; -;
 DR HSSP; P02577; 1NM1.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 SQ SEQUENCE 76 AA; 8276 MW; 996A861F69EA45DB CRC64;

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Query Match          100.0%; Score 83; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
Db 46 APPERKYSVWIGSI 60

RESULT 13
Q04947 PRELIMINARY; PRT; 76 AA.
AC Q04947;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Ipomoea nil (Japanese morning glory) (Pharbitis nil).
OS Ipomoea nil (Japanese morning glory) (Pharbitis nil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Convolvulaceae; Ipomoeaceae; Ipomoea.
OX NCBI_TaxID=35883;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Violet; TISSUE=Apical meristem;
RA Sage-Ono K., Ono M., Kanada H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D78205; BAAL1308.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1 76
FT SEQUENCE 76 AA; 8276 MW; 8BEDB60DB7A45DB CRC64;

Query Match          100.0%; Score 83; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
Db 46 APPERKYSVWIGSI 60

RESULT 14
Q04952 PRELIMINARY; PRT; 76 AA.
AC Q04952;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Ipomoea nil (Japanese morning glory) (Pharbitis nil).
OS Ipomoea nil (Japanese morning glory) (Pharbitis nil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Convolvulaceae; Ipomoeaceae; Ipomoea.
OX NCBI_TaxID=35883;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Violet; TISSUE=Apical meristem;
RA Sage-Ono K., Ono M., Kanada H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D78204; BAAL1307.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
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FT NON_TER 1 1
FT NON_TER 76 76
SQ SEQUENCE 76 AA; 8310 MW; C96A74451CED45C0 CRC64;

Query Match          100.0%; Score 83; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
Db 46 APPERKYSVWIGSI 60

RESULT 15
Q23875 PRELIMINARY; PRT; 83 AA.
AC Q23875;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Actin 2 sub 1 (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3;
RX MEDLINE=80101584; PubMed=293714;
RA Firtel R.A., Timm R., Kimmel A.R., McKeown M.;
RT "Unusual nucleotide sequences at the 5' end of actin genes in Dictyostelium discoideum.";
RL Dictyostelium discoideum.
RL Proc. Natl. Acad. Sci. U.S.A. 76:6206-6210(1979).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3;
RX MEDLINE=8212583; PubMed=6276562;
RA McKeown M., Firtel R.A.;
RT "Evidence for sub-families of actin genes in Dictyostelium as determined by comparisons of 3' end sequences.";
RL J. Mol. Biol. 151:593-606(1981).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3;
RX MEDLINE=82260445; PubMed=6286214;
RA McKeown M., Firtel R.A.;
RT "Actin multigene family of Dictyostelium.";
RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR EMBL; K02954; AAA33148.1; -.
DR HSSP; P02577; 1NM1.
DR DictyBase; DDB0185124; act2.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1 1
FT SEQUENCE 83 AA; 9149 MW; 2E0F415B2D075292 CRC64;

Query Match          100.0%; Score 83; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
Db 39 APPERKYSVWIGSI 53
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Job time : 58.8667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-15
Perfect score: 83
Sequence: 1 APPERKYSWIGGSI 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	47	3	US-09-306-446C-7
2	83	100.0	239	4	US-09-949-016-10409
3	83	100.0	374	3	US-08-609-236-6
4	83	100.0	374	2	US-09-306-446C-2
5	83	100.0	375	2	US-08-494-151-14
6	83	100.0	375	3	US-09-106-217-16
7	83	100.0	375	3	US-09-171-337A-7
8	83	100.0	375	4	US-09-631-022-7
9	83	100.0	375	4	US-09-976-594-731
10	83	100.0	376	1	US-08-588-113-2
11	83	100.0	376	4	US-09-949-016-6100
12	83	100.0	377	3	US-09-106-217-2
13	83	100.0	377	4	US-09-919-172-33
14	83	100.0	377	4	US-09-917-254-53
15	83	100.0	377	4	US-09-248-796A-14109
16	83	100.0	386	4	US-09-949-016-7721
17	83	100.0	399	4	US-09-949-016-9424
18	83	100.0	402	4	US-09-949-016-10757
19	83	100.0	404	4	US-09-949-016-11313
20	79	95.2	336	4	US-09-248-796A-14108
21	73	88.0	375	3	US-09-171-337A-8
22	73	88.0	375	4	US-09-631-022-8
23	68	81.9	384	4	US-09-538-092-395
24	66	79.5	30	4	US-09-270-767-5368
25	66	79.5	30	4	US-09-270-767-5368
26	64	77.1	362	4	US-09-949-016-7725
27	64	77.1	376	4	US-09-538-092-1109

ALIGNMENTS

RESULT 1

US-09-306-446C-7
; Sequence 7, Application US/09306446C
; Patent No. 6372959

GENERAL INFORMATION:

; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyoun Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344050/HAS
; CURRENT APPLICATION NUMBER: US/09/306,446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus

US-09-306-446C-7

Query Match 100.0%; Score 83; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGGSI 15
DB 3 APPERKYSWIGGSI 17

RESULT 2

US-09-949-016-10409
; Sequence 10409, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10409
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10409

Query Match      100.0%; Score 83; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels -0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
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DB 330 APPERKYSVWIGSI 344

RESULT 4
US-09-306-446C-2
; Sequence 2, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyou Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344US0/BAS
; CURRENT APPLICATION NUMBER: US/09/306,446C
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-2

Query Match      100.0%; Score 83; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGSI 15
   |||||
DB 330 APPERKYSVWIGSI 344

RESULT 5
US-08-494-151-14
; Sequence 14, Application US/08494151
; Patent No. 5840528
; GENERAL INFORMATION:
; APPLICANT: Van Ooyen, Albert Johannes Joseph
; TITLE OF INVENTION: Transformation of Phaffia rhodozyma
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,151
; FILING DATE: 23-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murahige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20039.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 14:

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SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-494-151-14

Query Match 100.0%; Score 83; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGGSI 15
Db 331 APPERKYSWIGGSI 345

RESULT 6

US-09-106-217-16
Sequence 16, Application US/09106217
Patent No. 6063576

GENERAL INFORMATION:

APPLICANT: Keating, Mark T.

APPLICANT: Olson, Timothy M.

TITLE OF INVENTION: Actin Mutations in Dilated

TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS: 18

ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.

STREET: 555 Thirteenth Street, N.W., Suite 701 East

CITY: Washington

STATE: DC

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/106,217

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Stephen A.

REGISTRATION NUMBER: 38,609

REFERENCE/DOCKET NUMBER: 2323-125

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-783-6040

TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-106-217-16

Query Match 100.0%; Score 83; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGGSI 15
Db 331 APPERKYSWIGGSI 345

RESULT 7

US-09-171-337A-7

Sequence 7, Application US/09171337A

Patent No. 6300095

GENERAL INFORMATION:

APPLICANT: BARREDO FUENTE, Jose Luis

RODRIGUEZ SAIZ, Marta
COLLADOS DE LA VIEJA, Alfonso J.
MORENO VALLE, Migeul Angel
SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno

TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: LADAS & PARRY

STREET: 26 WEST 61 STREET

CITY: NEW YORK

STATE: NY

COUNTRY: USA

ZIP: 10023

COMPUTER READABLE FORM:

MEDIUM TYPE: 3-1/4" Disk 1.44MB

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11

SOFTWARE: WordPerfect 8 for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/171,337A

FILING DATE: 14-May-1999

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/ES98/00056

FILING DATE: 5-MAR-1998

APPLICATION NUMBER: ES9700482

FILING DATE: 5-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: MASS, Clifford J.

REGISTRATION NUMBER: 30,086

TELECOMMUNICATION INFORMATION:

TELEPHONE: 233288

INFORMATION FOR SEQ ID NO: 7

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORGANISM: Penicillium chrysogenum

FEATURE:

OTHER INFORMATION: amino acid sequence of the -actin

protein with a molecular weight of

41760 Da.

SEQUENCE DESCRIPTION: SEQ ID NO: 7

US-09-171-337A-7

Query Match 100.0%; Score 83; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGGSI 15

Db 331 APPERKYSWIGGSI 345

RESULT 8

US-09-631-022-7

Sequence 7, Application US/09631022

Patent No. 6558921

GENERAL INFORMATION:

APPLICANT: BARREDO FUENTE, Jose Luis

RODRIGUEZ SAIZ, Marta

COLLADOS DE LA VIEJA, Alfonso J.

MORENO VALLE, Migeul Angel

SALTO MALDONADO, Francisco

DIEZ GARCIA, Bruno

;; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
;; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
;; AND -ACTIN AND THEIR USE IN FILAMENTOUS
;; FUNGI EXPRESSION, SECRETION AND ANTISENSE
;;
;; NUMBER OF SEQUENCES: 20
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LADAS & PARRY
;; STREET: 26 WEST 61 STREET
;; CITY: NEW YORK
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10023
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3-1/4" Disk 1.44MB
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
;; SOFTWARE: WordPerfect 8 for Windows
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/631,022
;; FILING DATE: 02-Aug-2000
;; CLASSIFICATION: 536
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/171,337
;; FILING DATE: 14-MAY-1999
;; APPLICATION NUMBER: PCT/ES98/00056
;; FILING DATE: 5-MAR-1998
;; APPLICATION NUMBER: ES9700482
;; FILING DATE: 5-MAR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MASS, Clifford J.
;; REGISTRATION NUMBER: 30,086
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 233288
;; INFORMATION FOR SEQ ID NO: 7
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 375 amino acids
;; TYPE: amino acids
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: Penicillium chrysogenum
;; FEATURE:
;; OTHER INFORMATION: amino acid sequence of the -actin
;; protein with a molecular weight of
;; 41760 Da.
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-09-631-022-7

Query Match 100.0%; Score 83; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGGSI 15
Db 331 APPERKYSVWIGGSI 345

RESULT 9
US-09-976-594-731
; Sequence 731, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143

;; SOFTWARE: PERL Program
;; SEQ ID NO 731
;; LENGTH: 375
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. 6673549 1837317CDI
US-09-976-594-731

Query Match 100.0%; Score 83; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGGSI 15
Db 331 APPERKYSVWIGGSI 345

RESULT 10
US-08-588-113-2
; Sequence 2, Application US/08588113
; Patent No. 5710003
; GENERAL INFORMATION:
; APPLICANT: McHugh, Kirk M.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5710003ria
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,113
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: TJU-1652
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-588-113-2

Query Match 100.0%; Score 83; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSVWIGGSI 15
Db 332 APPERKYSVWIGGSI 346

RESULT 11
US-09-949-016-6100
; Sequence 6100, Application US/09949016
; Patent No. 6812339

;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6100
;; LENGTH: 376
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-6100

Query Match 100.0%; Score 83; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSSI 15
|||
Db 332 APPERKYSVWIGSSI 346
|||

RESULT 12
US-09-106-217-2
;; Sequence 2, Application US/09106217
;; Patent No. 6063576
;; GENERAL INFORMATION:
;; APPLICANT: Keating, Mark T.
;; APPLICANT: Olson, Timothy M.
;; TITLE OF INVENTION: Actin Mutations in Dilated
;; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
;; NUMBER OF SEQUENCES: 18
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
;; STREET: 555 Thirteenth Street, N.W., Suite 701 East
;; STREET: Tower
;; CITY: Washington
;; STATE: DC
;; COUNTRY: U.S.A.
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/106,217
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saxe, Stephen A.
;; REGISTRATION NUMBER: 38,609
;; REFERENCE/DOCKET NUMBER: 2323-125
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-783-6040
;; TELEFAX: 202-783-6031
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 377 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-106-217-2

Query Match 100.0%; Score 83; DB 3; Length 377;

Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPERKYSVWIGSSI 15
|||
Db 333 APPERKYSVWIGSSI 347
|||
RESULT 13
US-09-919-172-33
;; Sequence 33, Application US/09919172
;; Patent No. 6673545
;; GENERAL INFORMATION:
;; APPLICANT: Farris, Mary
;; APPLICANT: Turner, Christopher M.
;; TITLE OF INVENTION: PROSTATE CANCER MARKERS
;; FILE REFERENCE: PA-0036 US
;; CURRENT APPLICATION NUMBER: US/09/919,172
;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/222,469
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: PERL Program
;; SEQ ID NO 33
;; LENGTH: 377
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. 6673545 1709118CDI
US-09-919-172-33

Query Match 100.0%; Score 83; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSSI 15
|||
Db 333 APPERKYSVWIGSSI 347
|||

RESULT 14
US-09-917-254-53
;; Sequence 53, Application US/09917254
;; Patent No. 6703204
;; GENERAL INFORMATION:
;; APPLICANT: Mutter, George
;; APPLICANT: Baak, Jan
;; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
;; FILE REFERENCE: B0801/7224(JRV)
;; CURRENT APPLICATION NUMBER: US/09/917,254
;; CURRENT FILING DATE: 2001-07-27
;; PRIOR APPLICATION NUMBER: US 60/222,093
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 53
;; LENGTH: 377
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 100.0%; Score 83; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSSI 15
|||
Db 333 APPERKYSVWIGSSI 347
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RESULT 15
US-09-248-796A-14109

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; Sequence 14109, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14109
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14109

Query Match      100.0%; Score 83; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 APPERKYSVWIGSI 15
      |||||||
Db      333 APPERKYSVWIGSI 347

Search completed: April 8, 2005, 12:07:40
Job time : 17.5333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds
(without alignments)
116.718 Million cell updates/sec

Title: US-09-423-351C-15

Perfect score: 83

Sequence: 1 APPERKYSVWIGSSI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	47	15 US-10-341-434-139	Sequence 139, App
2	83	100.0	57	16 US-10-437-963-172142	Sequence 172142, App
3	83	100.0	58	16 US-10-437-963-127939	Sequence 127939, App
4	83	100.0	67	16 US-10-437-963-194437	Sequence 194437, App
5	83	100.0	72	16 US-10-437-963-153523	Sequence 153523, App
6	83	100.0	74	16 US-10-767-701-33598	Sequence 33598, A
7	83	100.0	74	16 US-10-767-701-58873	Sequence 58873, A
8	83	100.0	81	15 US-10-424-599-157586	Sequence 157586, A
9	83	100.0	83	15 US-10-424-599-280813	Sequence 280813, A
10	83	100.0	89	15 US-10-424-599-158103	Sequence 158103, A
11	83	100.0	95	16 US-10-767-701-55472	Sequence 55472, A
12	83	100.0	100	9 US-09-796-692-1768	Sequence 1768, Ap
13	83	100.0	100	9 US-09-796-692-2271	Sequence 2271, Ap

14	83	100.0	100	14	US-10-040-862-1768	Sequence 1768, Ap
15	83	100.0	100	14	US-10-040-862-2271	Sequence 2271, Ap
16	83	100.0	100	15	US-10-057-4758-1768	Sequence 1768, Ap
17	83	100.0	100	15	US-10-057-4758-2271	Sequence 2271, Ap
18	83	100.0	100	15	US-10-154-884B-1768	Sequence 1768, Ap
19	83	100.0	100	15	US-10-154-884B-2271	Sequence 2271, Ap
20	83	100.0	100	16	US-10-764-324-1768	Sequence 1768, Ap
21	83	100.0	100	16	US-10-764-324-2271	Sequence 2271, Ap
22	83	100.0	101	9	US-09-925-300-1732	Sequence 1732, Ap
23	83	100.0	106	15	US-10-424-599-281378	Sequence 281378, Ap
24	83	100.0	110	15	US-10-264-049-4060	Sequence 4060, Ap
25	83	100.0	125	15	US-10-425-114-59245	Sequence 59245, A
26	83	100.0	129	9	US-09-796-692-2183	Sequence 2183, Ap
27	83	100.0	129	14	US-10-040-862-2183	Sequence 2183, Ap
28	83	100.0	129	15	US-10-057-4758-2183	Sequence 2183, Ap
29	83	100.0	129	15	US-10-154-884B-2183	Sequence 2183, Ap
30	83	100.0	129	16	US-10-764-324-2183	Sequence 2183, Ap
31	83	100.0	133	15	US-10-424-599-143033	Sequence 143033, Ap
32	83	100.0	135	15	US-10-424-599-157815	Sequence 157815, Ap
33	83	100.0	145	15	US-10-264-049-4259	Sequence 4259, Ap
34	83	100.0	147	9	US-09-796-692-1239	Sequence 1239, Ap
35	83	100.0	147	9	US-09-796-692-1696	Sequence 1696, Ap
36	83	100.0	147	9	US-09-796-692-2250	Sequence 2250, Ap
37	83	100.0	147	14	US-10-040-862-1239	Sequence 1239, Ap
38	83	100.0	147	14	US-10-040-862-1696	Sequence 1696, Ap
39	83	100.0	147	14	US-10-040-862-2250	Sequence 2250, Ap
40	83	100.0	147	15	US-10-057-4758-1239	Sequence 1239, Ap
41	83	100.0	147	15	US-10-057-4758-1696	Sequence 1696, Ap
42	83	100.0	147	15	US-10-057-4758-2250	Sequence 2250, Ap
43	83	100.0	147	15	US-10-154-884B-1239	Sequence 1239, Ap
44	83	100.0	147	15	US-10-154-884B-1696	Sequence 1696, Ap
45	83	100.0	147	15	US-10-154-884B-2250	Sequence 2250, Ap

ALIGNMENTS

RESULT 1
US-10-341-434-139
; Sequence 139, Application US/10341434
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; PRIORITY FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 139
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-139

Query Match 100.0%; Score 83; DB 15; Length 47;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSSI 15

Db 3 APPERKYSVWIGSSI 17

RESULT 2

US-10-437-963-172142
; Sequence 172142, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

RESULT 4
US-10-437-963-194437
; Sequence 194437, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

RESULT 6
US-10-767-701-33598
; Sequence 33598, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 33598

LENGTH: 74

TYPE: PRT

ORGANISM: Sorghum bicolor

FEATURE:

OTHER INFORMATION: Clone ID: SORBI-28MAY03-C33956_1.pep

US-10-767-701-33598

Query Match 100.0%; Score 83; DB 16; Length 74;

Best Local Similarity 100.0%; Pred. No. 9.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSSI 15

Db 30 APPERKYSVWIGSSI 44

RESULT 7

US-10-767-701-58873

Sequence 58873, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 58873

LENGTH: 74

TYPE: PRT

ORGANISM: Sorghum bicolor

FEATURE:

OTHER INFORMATION: Clone ID: 6676255.pep

US-10-767-701-58873

Query Match 100.0%; Score 83; DB 16; Length 74;

Best Local Similarity 100.0%; Pred. No. 9.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSSI 15

Db 30 APPERKYSVWIGSSI 44

RESULT 8

US-10-424-599-157586

Sequence 157586, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 157586

LENGTH: 81

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_11331C.1.pep

US-10-424-599-157586

Query Match 100.0%; Score 83; DB 15; Length 81;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSSI 15

Db 37 APPERKYSVWIGSSI 51

RESULT 9

US-10-424-599-280813

Sequence 280813, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 280813

LENGTH: 83

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_95597C.1.pep

US-10-424-599-280813

Query Match 100.0%; Score 83; DB 15; Length 83;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPERKYSVWIGSSI 15

Db 39 APPERKYSVWIGSSI 53

RESULT 10

US-10-424-599-158103

Sequence 158103, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 158103

LENGTH: 89

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(89)

OTHER INFORMATION: unsure at all Xaa locations

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; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-692-1768

Query Match      100.0%; Score 83; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APPERKYSVWIGSSI 15
        |||||||||
DB      76 APPERKYSVWIGSSI 90

RESULT 13
US-09-796-692-2271
; Sequence 2271, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-692-2271

Query Match      100.0%; Score 83; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-14
Perfect score: 75
Sequence: 1 APSTMKIKIAPP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	67	I46473	alpha-actin - rabb
2	75	100.0	125	A26337	actin, skeletal mu
3	75	100.0	155	A60945	actin homolog FAR,
4	75	100.0	232	I46679	alpha-smooth muscl
5	75	100.0	349	B25819	actin, fetal skele
6	75	100.0	362	A26559	actin type 5, cyto
7	75	100.0	374	ATB08	actin beta - bovin
8	75	100.0	374	ATB0G	actin gamma - bovi
9	75	100.0	374	JCS818	gamma-actin - huma
10	75	100.0	375	1 ATBOSM	actin, aortic smoo
11	75	100.0	375	1 ATRB	actin, skeletal mu
12	75	100.0	375	1 ATRC	actin beta - rat
13	75	100.0	375	1 A48324	actin beta, cytosk
14	75	100.0	375	1 ATAX	actin - Acanthamo
15	75	100.0	375	1 ATCHB	actin beta - chick
16	75	100.0	375	1 ATDO	actin - slime mold
17	75	100.0	375	1 ATHUB	actin beta - human
18	75	100.0	375	1 ATHUG	actin gamma 1 - hu
19	75	100.0	375	1 ATMSB	actin beta - mouse
20	75	100.0	375	1 ATMSG	actin gamma - mous
21	75	100.0	375	1 ATRBB	actin beta, non-mu
22	75	100.0	375	1 S11222	actin gamma, cytos
23	75	100.0	375	2 T25272	hypothetical prote
24	75	100.0	375	2 S71124	actin beta-1, cyto
25	75	100.0	375	2 S71126	actin beta, cytosk
26	75	100.0	375	2 A55001	actin beta - goose
27	75	100.0	375	2 A54728	actin alpha, cardi
28	75	100.0	376	1 ATFF7	actin 7 - fruit fl
29	75	100.0	376	1 A43552	actin gamma, cytos

30	75	100.0	376	1 ATCHSM	actin gamma, smoot
31	75	100.0	376	1 ATFY	actin - slime mold
32	75	100.0	376	2 B23412	actin 12 - slime m
33	75	100.0	376	2 A48449	Actin-1A - nematod
34	75	100.0	376	2 A40261	actin gamma, enter
35	75	100.0	376	2 C23412	actin 3-sub1 - sll
36	75	100.0	376	2 A25084	actin 15 - slime m
37	75	100.0	376	2 S27135	actin 4 - Caenorha
38	75	100.0	376	2 S16710	actin 1 and actin
39	75	100.0	376	2 S16709	actin 2 - Caenorha
40	75	100.0	376	2 T24448	hypothetical prote
41	75	100.0	376	2 JCS227	actin 1 - earthwor
42	75	100.0	376	2 S12730	actin - California
43	75	100.0	376	2 S11453	actin (clone 403)
44	75	100.0	376	2 S49481	actin 5 - Atlantic
45	75	100.0	376	2 S49479	actin 11 - Atlanti

ALIGNMENTS

RESULT 1

I46473
alpha-actin - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I46473
R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1993
A:Title: A new tropinin T and cDNA clones for 13 different muscle proteins, found by sh
A:Reference number: I46471; MUID:83167564; PMID:6687628
A:Accession: I46473
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-67 <PUI>
A:Cross-references: UNIPROT:P02568; EMBL:V00874; NID:gl432; PIDN:CAA24243.1; PID:g833379
C:Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APSTMKIKIAPP 15
Db 13 APSTMKIKIAPP 27

RESULT 2

A26337
actin, skeletal muscle - Iberian ribbed newt (fragment)
C:Species: Pleurodeles waltlii (Iberian ribbed newt)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A26337
R:Khrestchatisky, M.; Fontes, M.
J. Mol. Biol. 193, 409-412, 1987
A:Title: There is an alpha-actin skeletal muscle-specific gene in a salamander (Pleurod
A:Reference number: A26337; MUID:87254218; PMID:3453122
A:Accession: A26337
A:Molecule type: DNA
A:Residues: 1-125 <KHR>
A:Cross-references: UNIPROT:P10994; GB:X05106; NID:g64240; PIDN:CAA28753.1; PID:g64249
C:Superfamily: actin
C:Keywords: muscle; skeletal muscle

Query Match 100.0%; Score 75; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APSTMKIKIAPP 15
Db 71 APSTMKIKIAPP 85

Fri Apr 8 14:14:21 2005

us-09-423-351c-14.rpr

Best Local Similarity 100.0%; Pred. NO. 8.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APSTMKIKIAPP 15
Db 295 APSTMKIKIAPP 309

RESULT 6

A26559
actin type 5, cytosolic - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C:Accession: A26559
R:Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A:Reference number: A26559; MUID:85213487; PMID:4000121
A:Accession: A26559
A:Molecule type: DNA
A:Residues: 1-362 <BER>
C:Superfamily: actin
C:Keywords: cytosol; methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. NO. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APSTMKIKIAPP 15
Db 322 APSTMKIKIAPP 336

RESULT 7

ATBOB
actin beta - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A39105; A02999; A14185
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P60712
A:Note: only peptides that differed in composition from the corresponding peptides of r
R:Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A:Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analy
A:Reference number: A39105; MUID:84032385; PMID:6195151
A:Accession: A39105
A:Molecule type: mRNA
A:Residues: 76-227;344-374 <DEG>
A:Cross-references: GB:K00622; GB:K00623
A:Note: actins beta and gamma were not distinguished in this study
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. NO. 8.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APSTMKIKIAPP 15
Db 320 APSTMKIKIAPP 334

RESULT 8

RESULT 3
A60945
actin homolog FAT, testicular - starfish (Pisaster ochraceus) (fragments)
C:Species: Pisaster ochraceus
C:Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A60945
R:Boom, J.D.G.; Smith, M.J.
J. Exp. Zool. 250, 312-320, 1989
A:Title: Molecular analyses of gene expression during sea star spermatogenesis.
A:Reference number: A60945; MUID:89341660; PMID:2474626
A:Accession: A60945
A:Molecule type: mRNA
A:Residues: 1-155 <BOO>
A:Cross-references: UNIPROT:Q7M3Y6
A:Note: authors translated the codon TTG for residue 77 as Ile, and TGC for residue 81 a
C:Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. NO. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APSTMKIKIAPP 15
Db 124 APSTMKIKIAPP 138

RESULT 4

I46679
alpha-smooth muscle actin - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
C:Accession: I46679
R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
A:Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by sh
A:Reference number: I4671; MUID:83167564; PMID:6687628
A:Accession: I46679
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <PUT>
A:Cross-references: GB:J00654; NID:g164748; PIDN:AAA31154.1; PID:g164750
C:Genetics: 75/3; 165/3
A:Introns: 75/3; 165/3
C:Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. NO. 5.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APSTMKIKIAPP 15
Db 178 APSTMKIKIAPP 192

RESULT 5

B25819
actin, fetal skeletal/adult cardiac muscle - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: B25819
R:Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
J. Mol. Evol. 23, 11-22, 1986
A:Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
A:Reference number: A25819; MUID:86200234; PMID:3084797
A:Accession: B25819
A:Molecule type: mRNA
A:Residues: 1-349 <ALO>
A:Cross-references: UNIPROT:Q61275; GB:X03767; GB:J00381; GB:M10652; NID:g49869; PIDN:CA
C:Superfamily: actin
C:Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F:47/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 349;

ATBOG

actin gamma - bovine (tentative sequence)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: B14185; A02999
 R;Vandekerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
 A:Reference number: A14185; MUID:79045349; PMID:213279
 A:Accession: B14185
 A:Molecule type: protein
 A:Residues: 1-374 <VAN>
 A:Cross-references: UNIPROT:P02571
 A:Note: only peptides that differed in composition from the corresponding peptides of ra
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C:Superfamily: actin
 C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
 F;1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
 F;72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIIAPPER 15
 |||||
 Db 320 APSTMKIKIIAPPER 334

RESULT 9

JC5818
 gamma-actin - human
 C:Species: Homo sapiens (man)
 C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
 C:Accession: JC5818; PC4501
 R;Haenschltdt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens
 Biochem. Biophys. Res. Commun. 241, 670-674, 1997
 A:Title: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes
 A:Reference number: JC5818; MUID:98096379; PMID:9434766
 A:Accession: JC5818
 A:Molecule type: protein
 A:Residues: 1-374 <HAU>
 A:Cross-references: UNIPROT:P02571
 A:Experimental source: monocyte
 C:Comment: This protein is involved in a signal transduction that eventually leads to m
 C:Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIIAPPER 15
 |||||
 Db 320 APSTMKIKIIAPPER 334

RESULT 10

ATBOSM
 actin, aortic smooth muscle - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
 C:Accession: A02997; S13480
 R;Vandekerckhove, J.; Weber, K.
 Differentiation 14, 123-133, 1979
 A:Title: The complete amino acid sequence of actins from bovine aorta, bovine heart, bo
 tiation.
 A:Reference number: A02997; MUID:80047657; PMID:499690
 A:Accession: A02997
 A:Molecule type: protein

A:Residues: 1-375 <VAN>
 R;Zevgolis, V.G.; Sotiropoulos, T.G.; Evangelopoulos, A.E.
 Biochim. Biophys. Acta 1091, 222-230, 1991
 A:Title: Phosphorylase kinase from bovine stomach smooth muscle: a Ca(2+)-dependent pro
 A:Reference number: S13480; MUID:91137633; PMID:1995080
 A:Accession: S13480
 A:Molecule type: protein
 A:Residues: 40-49 <ZEV>
 A:Experimental source: stomach
 A:Note: this material appears to be actin of aortic smooth muscle type or a related mol
 C:Superfamily: actin
 C:Keywords: acetylated amino end; methylated amino acid; muscle contraction
 F;1/Modified site: acetylated amino end (Glu) #status predicted
 F;73/Modified site: 3'-methylhistidine (His) #status experimental
 Query Match 100.0%; Score 75; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 8.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APSTMKIKIIAPPER 15
 |||||
 Db 321 APSTMKIKIIAPPER 335

RESULT 11
 ATRB
 actin, skeletal muscle - rabbit
 N:Alternate names: F-actin
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-May-1999
 C:Accession: A92182; A14185; S65873; S70610; S44393; A02994
 R;Collins, J.H.; Elzinga, M.
 J. Biol. Chem. 250, 5915-5920, 1975
 A:Title: The primary structure of actin from rabbit skeletal muscle. Completion and ana
 A:Reference number: A92182; MUID:75211334; PMID:1150665
 A:Accession: A92182
 A:Molecule type: protein
 A:Residues: 1-2,'T','4','D','6-11','13-73','W','74-78,80-234,236-308','T','310-375 <COL>
 A:Note: this is the final paper in a series
 A:Note: this sequence has been revised in references A14185 and A90406
 R;Vandekerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brai
 A:Reference number: A14185; MUID:79045349; PMID:213279
 A:Accession: A14185
 A:Molecule type: protein
 A:Residues: 1-18;69-84 <VAN>
 R;Lu, R.C.; Elzinga, M.
 Biochemistry 16, 5801-5806, 1977
 A:Title: Partial amino acid sequence of brain actin and its homology with muscle actin.
 A:Reference number: A90406; MUID:78060866; PMID:588555
 A:Contents: annotation
 A:Note: residue 235 has been added and residue 309 has been revised
 R;Vahdat, A.; Miller, C.; Phillips, M.; Muhlrad, A.; Reisler, E.
 FEBS Lett. 365, 149-151, 1995
 A:Title: A novel 27/16 kDa form of subtilisin cleaved actin: structural and functional
 A:Reference number: S65873; MUID:95300963; PMID:7781768
 A:Accession: S65873
 A:Molecule type: protein
 A:Residues: 235-241 <VAH>
 R;Strzelecka-Golaszewska, H.; Wozniak, A.; Hult, T.; Lindberg, U.
 Biochem. J. 316, 713-721, 1996
 A:Title: Effects of the type of divalent cation, Ca2+ or Mg2+, bound at the high-affini
 A:Reference number: S70610; MUID:96265033; PMID:8670143
 A:Accession: S70610
 A:Molecule type: protein
 A:Residues: 48-54;68-72;235-243 <STR>
 A:Experimental source: skeletal muscle
 R;Bertrand, R.; Derancourt, J.; Kassab, R.
 FEBS Lett. 345, 113-119, 1994
 A:Title: The covalent maleimidebenzoyl-actin-myosin head complex. Cross-linking of the
 A:Reference number: S44393; MUID:94259162; PMID:8200441
 A:Accession: S44393

A:Molecule type: protein
A:Residues: 48-64 <BER>
A:Experimental source: skeletal muscle
C:Superfamily: actin
C:Keywords: acetylated amino end; ATP binding; methylated amino acid; muscle contraction
F:1-375/Product: actin #status experimental <MAT>
F:1/Modified site: acetylated amino end (Asp) #status experimental
F:73/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
|||||
DB 321 APSTMKIKIAPP 335

RESULT 12
ATRTC
actin beta - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
C:Accession: A38571; A02999
R:Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A:Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A:Reference number: A38571; MUID:83168920; PMID:6300777
A:Accession: A38571
A:Molecule type: DNA
A:Residues: 1-375 <NUD>
A:Cross-references: GB:J00691; NID:g202653; PIDN:AAA40657.1; PID:g202654
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Genetics:
A:Introns: 41/3; 121/3; 268/1; 328/3
C:Superfamily: actin
C:Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;
F:2-375/Product: actin beta #status predicted <MAT>
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
|||||
DB 321 APSTMKIKIAPP 335

RESULT 13
A48324
actin beta, cytoskeletal - common carp
C:Species: Cyprinus carpio (common carp)
C:Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: A48324
R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
DNA Seq. 1, 125-136, 1990
A:Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A:Reference number: A48324; MUID:92190540; PMID:2134183
A:Accession: A48324
A:Molecule type: DNA
A:Residues: 1-375 <LIU>
A:Cross-references: UNIPROT:P83750; GB:M24113; NID:g213041; PIDN:AAA6886.1; PID:g213042
A:Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 as Pro
A:Note: the authors failed to translated the codon GGT for residue 42 as Gly
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Genetics:
A:Introns: 41/3; 121/3; 268/3; 328/3
C:Superfamily: actin
C:Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F:2-375/Product: actin beta, cytoskeletal #status predicted <MAT>
F:73/Modified site: acetylated amino end (Asp) (in mature form) #status predicted

F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
|||||
DB 321 APSTMKIKIAPP 335

RESULT 14
ATAX

actin - Acanthamoeba castellanii
C:Species: Acanthamoeba castellanii
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A92886; A03004
R:Neilen, W.; Gallwitz, D.
J. Mol. Biol. 159, 1-18, 1982
A:Title: Actin genes and actin messenger RNA in Acanthamoeba castellanii. Nucleotide se
A:Reference number: A92886; MUID:83033627; PMID:6290670
A:Accession: A92886
A:Molecule type: DNA
A:Residues: 1-375 <NEU>
A:Cross-references: UNIPROT:P02578; GB:V00002; GB:J01016; NID:95565; PIDN:CAA23399.1; P
C:Comment: There are at least three actin genes in A. castellanii.
C:Genetics:
A:Introns: 105/3
C:Superfamily: actin
C:Keywords: methylated amino acid
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
|||||
DB 321 APSTMKIKIAPP 335

RESULT 15
ATCB

actin beta - chicken
C:Species: Gallus gallus (chicken)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A20888; I50154
R:Kost, T.A.; Theodorakis, N.; Hughes, S.H.
Nucleic Acids Res. 11, 8287-8301, 1983
A:Title: The nucleotide sequence of the chick cytoplasmic beta-actin gene.
A:Reference number: A20888; MUID:84169478; PMID:6324080
A:Accession: A20888
A:Molecule type: DNA
A:Residues: 1-375 <KOS>
A:Cross-references: UNIPROT:P60706; EMBL:X00182
A:Note: the sequence shown follows the authors' translation at position 336
R:Chang, K.
Mol. Cell. Biol. 4, 2498-2508, 1984

A:Title: Isolation and characterization of six different chicken actin genes.
A:Reference number: I50153; MUID:85085956; PMID:6513927

A:Accession: I50154

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-17 <CHA>

A:Cross-references: GB:K02259; NID:g211086; PIDN:AAA48572.1; PID:g211087

C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Genetics:
A:Introns: 41/3; 121/3; 268/1; 328/3

C:Superfamily: actin

C:Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; m

F:2-375/Product: actin beta #status predicted <MAT>

F:73/Modified site: acetylated amino end (Asp) (in mature form) #status predicted

F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 8.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APSTMKIKIIAPPER 15
 |||||
 Db 321 APSTMKIKIIAPPER 335

Search completed: April 8, 2005, 10:53:08
 Job time : 9.33333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-14

Perfect score: 75
Sequence: 1 APSTMKIKIAPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	50	2 Q9DDZ2	Q9ddz2 micropterus
2	75	100.0	55	2 Q6LEI3	Q6lei3 dictyosteli
3	75	100.0	55	2 Q8AV69	Q8av69 oncorhynch
4	75	100.0	56	2 Q57575	Q57575 cynops pyrr
5	75	100.0	60	2 Q95164	Q95164 canis fami
6	75	100.0	61	2 Q23877	Q23877 dictyosteli
7	75	100.0	65	2 Q23878	Q23878 dictyosteli
8	75	100.0	83	2 Q23875	Q23875 dictyosteli
9	75	100.0	87	2 Q23879	Q23879 dictyosteli
10	75	100.0	88	2 Q23880	Q23880 dictyosteli
11	75	100.0	93	2 Q7Z220	Q7zz20 anas platyr
12	75	100.0	96	2 Q90X51	Q90x51 fundulus he
13	75	100.0	100	2 Q9TYD9	Q9tyd9 styela clav
14	75	100.0	103	2 Q95Y65	Q95y65 apis cerana
15	75	100.0	106	2 Q80UA7	Q80ua7 marmota mon
16	75	100.0	107	2 Q8J1Q2	Q8jiq2 anguilla ja
17	75	100.0	111	2 Q6R127	Q6r127 boophilus m
18	75	100.0	111	2 Q6R128	Q6r128 boophilus m
19	75	100.0	118	2 Q9DF22	Q9df22 scyllorhinu
20	75	100.0	123	2 Q6UIS1	Q6uis1 macaca mula
21	75	100.0	123	2 Q6UIS2	Q6uis2 pan troglod
22	75	100.0	124	2 Q9DFK3	Q9dfk3 gillichhys
23	75	100.0	125	1 ACT5_FLEWA	FI0994 pleurodeles
24	75	100.0	131	2 Q9XSB1	Q9xsb1 tupaiia glis
25	75	100.0	134	2 Q99NC5	Q99nc5 mus musculu
26	75	100.0	134	2 Q99NC6	Q99nc6 rattus norv
27	75	100.0	141	2 Q6PT58	Q6pt58 squalus aca
28	75	100.0	141	2 Q6Q5W9	Q6q6w9 ictalurus p
29	75	100.0	145	2 Q6B9V8	Q6b9v8 strongyloid
30	75	100.0	155	2 Q7M3Y6	Q7m3y6 pisaster oc
31	75	100.0	159	2 Q96DE1	Q96de1 homo sapien

32 75 100.0 159 2 Q9DG95 Q9dg95 pagrus majo
33 75 100.0 165 2 Q96F06 Q96f06 homo sapien
34 75 100.0 171 2 Q6GXE6 Q6gx66 lepisosteus
35 75 100.0 171 2 Q7ZWS9 Q7zw59 rana catesb
36 75 100.0 181 2 Q6XJ33 Q6xj33 drosophila
37 75 100.0 183 2 Q9YGY6 Q9ygy6 oreochromis
38 75 100.0 212 2 Q9GR83 Q9gr83 octopus vul
39 75 100.0 214 2 Q86PP6 Q86pp6 laodelphax
40 75 100.0 215 2 Q819K0 Q819k0 meloidogyne
41 75 100.0 215 2 Q819K1 Q819k1 meloidogyne
42 75 100.0 219 2 Q93402 Q93402 carassius a
43 75 100.0 235 2 Q28937 Q28937 sus scrofa
44 75 100.0 243 2 Q8MVP7 Q8mvp7 boltenia vi
45 75 100.0 245 2 Q9FUV2 Q9fuv2 gonionomas

ALIGNMENTS

RESULT 1
Q9DDZ2 PRELIMINARY; PRT; 50 AA.
AC Q9DDZ2; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Micropterus salmoides (Largemouth bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Centrarchidae; Micropterus.
OX NCBI_TaxID=27706;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Bowman C.J., Sabo-Attwood T.L., Lee H.S., Denslow N.D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP253319; AAG44624.1; --
DR HSSP; P02568; IMA9.
DR GO; GO:001529; C-actin cytoskeleton; IEA.
DR GO; GO:0005200; F-structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin-like.
FT NON_TER 1 1
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5694 MW; 44542890573899BB CRC64;
Query Match 100.0%; Score 75; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
DB 10 APSTMKIKIAPP 24

RESULT 2
Q6LEI3 PRELIMINARY; PRT; 55 AA.
AC Q6LEI3;
ID Q6LEI3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin 2 sub 2 (fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3;
RX MEDLINE=80101584; PubMed=293714;
RA Firtel R.A., Timm R., Kimmel A.R., McKeown M.;

RT "Unusual nucleotide sequences at the 5' end of actin genes in
 RL Dictyostelium discoideum";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:6206-6210(1979).
 (2)

RP SEQUENCE FROM N.A.
 RC STRAIN=A3;
 RX MEDLINE=82122583; PubMed=6276562;
 RA McKewon M., Firtel R.A.;
 RL "Evidence for sub-families of actin genes in Dictyostelium as
 RT determined by comparisons of 3' end sequences.";
 RL J. Mol. Biol. 151:593-606(1981).
 (3)

RP SEQUENCE FROM N.A.
 RC STRAIN=A3;
 RX MEDLINE=82260445; PubMed=6286214;
 RA McKewon M., Firtel R.A.;
 RL "Actin multigene family of Dictyostelium";
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
 DR EMBL; K02955; AAR23117.1; -;
 DR DictyBase; DDB0185125; act17.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR PROSITE; PS00432; ACTINS_2; 1.
 FT NON_TER 1
 FT SEQUENCE 55 AA; 6277 MW; F932FEB649E466CC CRC64;

Query Match 100.0%; Score 75; DB 2; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

Qy 1 APSTMKIKIAPP 15
 Db 1 APSTMKIKIAPP 15

RESULT 3

ID Q8AY69 PRELIMINARY; PRT; 55 AA.
 AC Q8AY69;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-actin (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Schwindt A.R., Alonso M., Leong J.C., Schreck C.B.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF550583; AAN74801.1; -;
 DR HSSP; P02568; IMA9.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 FT NON_TER 55
 FT SEQUENCE 55 AA; 6163 MW; 9A4319FB34DD79DB CRC64;

Query Match 100.0%; Score 75; DB 2; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

Qy 1 APSTMKIKIAPP 15
 Db 15 APSTMKIKIAPP 29

RESULT 4

ID O57575 PRELIMINARY; PRT; 56 AA.
 AC O57575;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Alpha cardiac actin (Fragment).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.;
 RL "pax-6 gene expression in newt eye development";
 RL Dev. Genes Evol. 207:167-176(1997).
 DR EMBL; D64017; BAA24031.1; -;
 DR HSSP; P02568; ILCU.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PROSITE; PS00432; ACTINS_2; 1.
 FT NON_TER 1
 FT SEQUENCE 56 AA; 6339 MW; 3532A4205AC550E5 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

Qy 1 APSTMKIKIAPP 15
 Db 2 APSTMKIKIAPP 16

RESULT 5

ID Q95164 PRELIMINARY; PRT; 60 AA.
 AC Q95164;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-actin (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97008128; PubMed=8855304; DOI=10.1073/pnas.93.20.11035;
 RA Lee Y.A., Liang C.S., Lee M.A., Lindpaintner K.;
 RL "Local stress, not systemic factors, regulate gene expression of the
 RT cardiac renin-angiotensin system in vivo: a comprehensive study of all
 RT its components in the dog";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11035-11040(1996).
 DR EMBL; U67202; RAC48640.1; -;
 DR HSSP; P02568; IMA9.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 FT NON_TER 60
 FT SEQUENCE 60 AA; 6744 MW; AA02DE065D32D7C4 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

Qy 1 APSTMKIKIAPP 15
 Db 15 APSTMKIKIAPP 29

RX MEDLINE=82260445; PubMed=6286214;
 RA McKeown M., Fittel R.A.;
 RT "actin multigene family of Dictyostelium.";
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505 (1982).
 DR ENBL; K02954; AAA33148.1; --
 DR HSPSP; P02577; INM1.
 DR DictyBase; DDB0185124; act2.
 DR GO:0005884; C:actin filament; IEA.

Fri Apr 8 14:14:21 2005

us-09-423-351c-14.rup

```

DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 83 AA; 9149 MW; 2E0F415B2D075292 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
DB 29 APSTMKIKIAPP 43

RESULT 9
Q23879 PRELIMINARY; PRT; 87 AA.
ID Q23879
AC Q23879;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Actin 8 (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=82122583; PubMed=6276562;
McKeown M., Firtel R.A.;
"Evidence for sub-families of actin genes in Dictyostelium as
determined by comparisons of 3' end sequences.";
J. Mol. Biol. 151:593-606(1981).
DR EMBL; J01278; AAA33157.1; -.
DR HSSP; P02577; 1NM1.
DR DictyBase; DDB0185015; act15.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 88 AA; 9776 MW; 29E270110E0A55D1 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
DB 34 APSTMKIKIAPP 48

RESULT 11
Q23880 PRELIMINARY; PRT; 88 AA.
ID Q23880;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Slime mold (D.discoideum) actin (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=82122583; PubMed=6276562;
McKeown M., Firtel R.A.;
"Evidence for sub-families of actin genes in Dictyostelium as
determined by comparisons of 3' end sequences.";
J. Mol. Biol. 151:593-606(1981).
DR EMBL; J01278; AAA33157.1; -.
DR HSSP; P02577; 1NM1.
DR DictyBase; DDB0185015; act15.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 93 AA; 10444 MW; F867ADF144D80523 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
DB 33 APSTMKIKIAPP 47

RESULT 10
Q23880 PRELIMINARY; PRT; 93 AA.
ID Q23880;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Spleen;
Sreekumar E., Premraj A., Rasool T.J.;
Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251275; AAP04479.1; -.
DR HSSP; P02568; 1QZ5.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 93 AA; 10444 MW; F867ADF144D80523 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
DB 33 APSTMKIKIAPP 47

```

Db 39 APSTMKIKIAPP 53

RESULT 12

Q90X51 ID Q90X51 PRELIMINARY; PRT; 96 AA.
AC Q90X51, 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Roling J.A., Baldwin W.S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF435092; AAL29465.1; -
DR HSP; P02568; 1Q25.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1 96
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10798 MW; 7440DA6A5A070C4 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15

Db 53 APSTMKIKIAPP 67

RESULT 13

Q9TYD9 ID Q9TYD9 PRELIMINARY; PRT; 100 AA.
AC Q9TYD9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-muscle actin (Fragment).
GN Names=Tb24;
OS Styela clava (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92249656; PubMed=1577198;
RA Beach R.L., Jeffery W.R.;
RT "Multiple actin genes encoding the same alpha-muscle isoform are expressed during ascidian development.";
RL Dev. Biol. 151:55-66(1992).
DR EMBL; L13788; AAA29846.1; -
DR HSP; P02568; 1Q25.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1 100
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 11264 MW; 108CE34548BABB5E CRC64;

Query Match 100.0%; Score 75; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15

Db 46 APSTMKIKIAPP 60

RESULT 14

Q95YG5 ID Q95YG5 PRELIMINARY; PRT; 103 AA.
AC Q95YG5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimizu I., Kawai Y., Taniguchi M., Aoki S.;
RT "Circadian rhythm and cDNA cloning of the clock gene period in the honeybee Apis cerana japonica";
RL Zool. Sci. 18:779-789(2001).
DR EMBL; AB072495; BAB69483.1; -
DR HSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1 103
FT NON_TER 103 103
SQ SEQUENCE 103 AA; 11520 MW; 5203DA3630FCD807 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15

Db 86 APSTMKIKIAPP 100

RESULT 15

Q80UA7 ID Q80UA7 PRELIMINARY; PRT; 106 AA.
AC Q80UA7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22554704; PubMed=12668969; DOI=10.1053/jhep.2003.50154;
RA Wang Y., Menne S., Jacob J.R., Tennant B.C., Gerin J.L., Cote P.J.;
RT "Role of type 1 versus type 2 immune responses in liver during the onset of chronic woodchuck hepatitis virus infection";
RL Hepatology 37:771-780(2003).
DR EMBL; AY170121; AAO39434.1; -
DR HSP; P10983; 1D4X.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.

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DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF0022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 106 AA; 11864 MW; 9FFDC145651FE343 CRC64;
Query Match 100.0%; Score 75; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APSTWKIKIAPP 15
Db 52 APSTWKIKIAPP 66

Search completed: April 8, 2005, 12:03:14
Job time : 57.8667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-15

Perfect score: 83

Sequence: 1 APPERKYSWIGGSI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	83	100.0	15	2 AAW92541	Beta-acti
2	83	100.0	15	4 AAB45796	Human aut
3	83	100.0	63	3 AAG18764	Zea mays
4	83	100.0	63	3 AAG32669	Zea mays
5	83	100.0	63	3 AAG32669	Zea mays
6	83	100.0	71	3 AAG32668	Zea mays
7	83	100.0	71	3 AAG37983	Arabidops
8	83	100.0	71	3 AAG48400	Arabidops
9	83	100.0	71	3 AAG18763	Zea mays
10	83	100.0	85	3 AAG48399	Arabidops
11	83	100.0	85	3 AAG37314	Arabidops
12	83	100.0	86	4 ABG08617	Novel hum
13	83	100.0	88	3 AAG37313	Arabidops
14	83	100.0	91	3 AAG18762	Zea mays
15	83	100.0	91	3 AAG37981	Arabidops
16	83	100.0	100	4 AAM81404	Human hae
17	83	100.0	100	4 AAM81907	Human hae
18	83	100.0	101	3 AAB57154	Human pro
19	83	100.0	107	3 AAG26469	Arabidops
20	83	100.0	107	3 AAG47776	Arabidops
21	83	100.0	107	3 AAG48382	Arabidops
22	83	100.0	110	3 AAG47775	Arabidops
23	83	100.0	110	5 ABP42928	Human ova
24	83	100.0	129	4 AAM81819	Human hae
25	83	100.0	145	5 ABP43127	Human ova

26	83	100.0	147	4 AAM80875	Human hae
27	83	100.0	147	4 AAM81886	Human hae
28	83	100.0	147	4 AAM81332	Human hae
29	83	100.0	149	8 ABO84771	Human can
30	83	100.0	164	3 AAG37312	Arabidops
31	83	100.0	177	3 AAG48381	Arabidops
32	83	100.0	181	4 ABG11441	Novel hum
33	83	100.0	186	3 AAG38701	Arabidops
34	83	100.0	186	3 AAG47774	Arabidops
35	83	100.0	186	3 AAG48380	Arabidops
36	83	100.0	229	3 AAG38700	Arabidops
37	83	100.0	246	3 AAG38699	Arabidops
38	83	100.0	257	3 AAG37992	Arabidops
39	83	100.0	257	3 AAG20916	Arabidops
40	83	100.0	274	6 ABU70549	Human adi
41	83	100.0	294	3 AAG20915	Arabidops
42	83	100.0	294	3 AAG37991	Arabidops
43	83	100.0	294	7 AD163068	Human apo
44	83	100.0	295	3 AAG20914	Arabidops
45	83	100.0	295	3 AAG37990	Arabidops

ALIGNMENTS

RESULT 1
AAW92541
ID AAW92541 standard; peptide; 15 AA.
XX
AC AAW92541;
XX
DT 26-APR-1999 (first entry)
XX
DE Beta-actin reference peptide substrate #15.
XX
KW Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
binding agent; substrate-binding site; SBS; substrate folding; actin;
tubulin; treatment; cancer; anticancer drug; viral infection; screening;
reduced toxicity.
XX
OS Synthetic.
XX
PN WO9853322-A1.
XX
PD 26-NOV-1998.
XX
PF 22-MAY-1998; 98WO-GB001485.
XX
PR 23-MAY-1997; 97GB-00010762.
XX
(CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.
XX
PI Willison K, Hynes G, Liou AK;
WPI; 1999-070162/06.
XX
PT Identifying specific binding agents for substrate binding site in CCT
chaperonin complex - also new peptide binding agents and their mimetics,
and peptides containing a specific CCT binding site, used for treating
cancer.
XX
PS Disclosure; Fig 10; 97pp; English.
XX
CC This invention describes a method which uses the CCT (eukaryotic type II
chaperonin) complex or part of it, for identifying a binding agent that
can occupy a substrate-binding site (SBS) on the CCT complex. By binding
to the CCT complex, the binding agents block an SBS so that biological
activity of the CCT complex is affected, particularly its ability to fold
substrates such as actin, tubulin and cyclin. The binding agents are
useful for treatment of cancer, particularly when used in combination
with an anticancer drug, or viral infections. Nucleic acid fragments are
used to screen for agents, e.g. binding agents that modulate interaction
between the CCT complex and a protein that is to be folded. The binding

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CC agents may target cells that are actively synthesizing tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AA92527-W92541 are
 CC peptide substrates used in the method of the invention

XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 83; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1 APPERKYSWIGGSI 15
 ID AAB45796 standard; peptide; 15 AA.
 AC AAB45796;
 XX 15-MAR-2001 (first entry)

DE Human autoantigen actin derived peptide #7.
 XX Actin; autoantigen; diagnostic; type 1 autoimmune hepatitis; virucide;
 KW immunodominant epitope; anti-idiotypic antibody; hepatotropic; vaccine;
 KW antiinflammatory; immunosuppressant; cirrhosis; human.

XX Homo sapiens.
 XX DE10002892-A1.
 XX 23-NOV-2000.

XX 11-JAN-2000; 2000DE-01002892.
 XX 12-JAN-1999; 99DE-01001503.
 XX (INTE-) INTEC IMMUNODIAGNOSTIKA GMBH.

XX Orth T, Schoessler W, Hentschel C;
 XX WPI; 2001-050680/07.
 XX New immunodominant peptides from actin, useful for diagnosis and
 XX treatment of type I autoimmune hepatitis.

XX Claim 3; Page 7; 8pp; German.
 XX This invention describes novel immunodominant peptides (I) from the
 XX autoantigen actin containing 10-20 amino acids and can bind to
 XX autoantibodies present in patients with type I autoimmune hepatitis. The
 XX invention also describes (1) antibodies (Ab) against immunodominant
 XX epitopes of actin that recognize at least one (1); (2) anti-idiotypic
 XX antibodies (Ab1) directed against Ab and recognizing specific types of Ab
 XX ; and (3) a test kit for determining anti-autoimmune hepatitis type 1
 XX antibodies in biological fluids comprising at least one of (1), conjugate
 XX of (1) with a carrier molecule or Ab1, adsorbed on, or covalently bonded
 XX to, a solid phase. The peptides of the invention have virucide,
 XX hepatotropic, antiinflammatory and immunosuppressant activity. (I) are
 XX useful in antigenic compositions to generate antibodies able to react
 XX specifically with autoantibodies, for detecting autoantibodies in
 XX biological fluids in standard immunoassays (anti-idiotypic antibodies or
 XX against antibodies raised to (I) can be used similarly), for diagnosis or
 XX monitoring of type 1 autoimmune hepatitis, in pharmaceutical compositions
 XX for treating type 1 autoimmune hepatitis and in vaccines for inducing
 XX tolerance. (I) provide a reliable, rapid and relatively simple diagnosis
 XX of type 1 autoimmune hepatitis. Early diagnosis of autoimmune hepatitis,
 XX which can be treated with immunosuppressants, is important to prevent
 XX progression to cirrhosis

SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1 APPERKYSWIGGSI 15
 ID AAG18764 standard; protein; 63 AA.
 AC AAG18764;
 XX 17-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 20302.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence; corn.

XX Zea mays subsp. mays.
 XX EPI033405-A2.
 XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.
 XX 25-FEB-1999; 99US-0121825P.
 XX 05-MAR-1999; 99US-0123180P.
 XX 09-MAR-1999; 99US-0123548P.
 XX 23-MAR-1999; 99US-0125788P.
 XX 25-MAR-1999; 99US-0126264P.
 XX 29-MAR-1999; 99US-0126785P.
 XX 01-APR-1999; 99US-0127462P.
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 XX 05-MAY-1999; 99US-0132485P.
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 XX 08-JUN-1999; 99US-0138094P.

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 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence; corn.
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Query Match 100.0%; Score 83; DB 3; Length 63;

Best Local Similarity 100.0%; Pred. No. 8e-06;

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DT 18-OCT-2000
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Query Match 100.0%; Score 83; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 8e-06;
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Qy 1 APPERKYSVWIGGSI 15
Db 19 APPERKYSVWIGGSI 33

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protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.

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Query Match 100.0%; Score 83; DB 3; Length 71;
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Qy 1 APPERKYSVWIGSI 15
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 Db 27 APPERKYSVWIGSI 41

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DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 61115.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

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Query Match      100.0%; Score 83; DB 3; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APPERKYSVWIGGSI 15
DB      27 APPERKYSVWIGGSI 41

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DT 17-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
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XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 61114.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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XX AC
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XX DT 18-OCT-2000 (first entry)
XX DE
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX PD
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Db 63 APPERKYSVWIGSI 77

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AC ABG08617;
XX
DT 13-FEB-2002 (first entry)
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DE Novel human diagnostic protein #8608.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS72804.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 38976; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations

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Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPERKYSWIGSSI 15
Db |||||
47 APPERKYSWIGSSI 61

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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PN EP1033405-A2.
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PD 06-SEP-2000.
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Query Match 100.0%; Score 83; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.2e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1 APPERYSVWIGGI 15
Db 47 APPERYSVWIGGI 61

Search completed: April 8, 2005, 10:50:51
Job time : 63.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-13
Perfect score: 73
Sequence: 1 ASSSSLEKSYELPDG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	73	100.0	92	2 A31409	actin - California
3	73	100.0	232	2 I46679	alpha-smooth muscul
4	73	100.0	308	2 A03000	actin 3 - fruit fl
5	73	100.0	328	2 S05430	actin beta - grass
6	73	100.0	349	2 B25819	actin, fetal skele
7	73	100.0	362	2 A26559	actin type 5, cyto
8	73	100.0	365	2 A37431	actin, type 1 - Em
9	73	100.0	374	1 ATBOH	actin beta - bovin
10	73	100.0	374	1 ATBOG	actin gamma - bovi
11	73	100.0	374	2 JCS818	gamma-actin - huma
12	73	100.0	375	1 ATBOSM	actin, aortic smoo
13	73	100.0	375	1 ATRB	actin, skeletal mu
14	73	100.0	375	1 ATRFC	actin beta - rat
15	73	100.0	375	1 A48324	actin beta, cytosk
16	73	100.0	375	1 ATCHB	actin beta - chick
17	73	100.0	375	1 ATCHUB	actin beta - human
18	73	100.0	375	1 ATHUG	actin gamma 1 - hu
19	73	100.0	375	1 ATMSB	actin beta - mouse
20	73	100.0	375	1 ATMSG	actin gamma - mous
21	73	100.0	375	1 ATRBB	actin beta, non-mu
22	73	100.0	375	1 S11222	actin gamma, cytos
23	73	100.0	375	2 T25272	hypothetical prote
24	73	100.0	375	2 S71125	actin beta-2, cyto
25	73	100.0	375	2 S71124	actin beta-1, cyto
26	73	100.0	375	2 A55001	actin beta - goose
27	73	100.0	375	2 A54728	actin alpha, cardi
28	73	100.0	376	1 A43552	actin gamma, cytos
29	73	100.0	376	1 ATCHSM	actin gamma, smoot

30 73 100.0 376 1 ATURS
31 73 100.0 376 2 A48449
32 73 100.0 376 2 JS0189
33 73 100.0 376 2 S07288
34 73 100.0 376 2 S09578
35 73 100.0 376 2 A40261
36 73 100.0 376 2 JQ0154
37 73 100.0 376 2 JN0833
38 73 100.0 376 2 A44940
39 73 100.0 376 2 S27135
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41 73 100.0 376 2 S16709
42 73 100.0 376 2 T24448
43 73 100.0 376 2 JCS227
44 73 100.0 376 2 S12730
45 73 100.0 376 2 S43509

actin CyI - sea ur
Actin-1A - nematod
actin, cytosolic -
actin 15A - sea ur
actin - sea urchin
actin gamma, ente
actin - Hydra atte
actin (clones Ia a
actin - pork tapew
actin 4 - Caenorha
actin 1 and actin
hypothetical prote
actin 1 - earthwor
actin - California
actin - California

ALIGNMENTS

RESULT 1

I46472
alpha-actin - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46472
R;Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1993
A;Title: A new tropinin T and cDNA clones for 13 different muscle proteins, found by sh-
A;Reference number: I46471; MUID:83167564; PMID:6687628
A;Accession: I46472
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-90 <PUT>
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C;Superfamily: actin

Query Match 100.0%; Score 73; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
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DB 40 ASSSSLEKSYELPDG 54

RESULT 2

A31409
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C;Species: Aplysia californica (California sea hare)
C;Date: 31-Mar-1990 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A31409; A60977
R;Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A;Title: Sequencing of proteins from two-dimensional gels by using in situ digestion an-
tion in Aplysia.
A;Reference number: A94207; MUID:88320566; PMID:3413132
A;Accession: A31409
A;Molecule type: protein
A;Residues: 1-18;21-92 <KEN>
A;CROSS-references: UNIPROT:Q7M3Y5
R;Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A;Title: Development of a database of amino acid sequences for proteins identified and
A;Reference number: A60977; MUID:89276264; PMID:2731514
A;Accession: A60977
A;Molecule type: protein
A;Residues: 1-20 <SWE>
C;Superfamily: actin

Query Match 100.0%; Score 73; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;

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us-09-423-351c-13.rpr

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 DB 60 ASSSSLEKSYELPDG 74

RESULT 3
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 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
 C:Accession: I46679
 R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.
 Nature 302, 718-721, 1983
 A:Title: A new tropomyosin T and cDNA clones for 13 different muscle proteins, found by shot
 A:Reference number: I46471; MUID:83167564; PMID:6687628
 A:Accession: I46679
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-232 <PUT>
 A:Cross-references: GB:J00654; NID:G164748; PIDN:AAA31154.1; PID:G164750
 C:Genetics:
 A:Introns: 75/3; 165/3
 C:Superfamily: actin

Query Match 100.0%; Score 73; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 DB 115 ASSSSLEKSYELPDG 129

RESULT 4
 A03000
 actin 3 - fruit fly (Drosophila melanogaster) (fragments)
 C:Species: Drosophila melanogaster
 C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C:Accession: A03000
 R:Fyberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
 Cell 24, 107-116, 1981
 A:Title: The actin genes of Drosophila: protein coding regions are highly conserved but
 A:Reference number: A03000; MUID:81210174; PMID:6263481
 A:Accession: A03000
 A:Molecule type: DNA
 A:Residues: 1-308 <FYB>
 A:Cross-references: UNIPROT:P02572
 A:Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequenc
 A:Note: the authors translated the codon GTT for residue 263 as Ile
 C:Genetics:
 A:Gene: FlyBase:Act42A
 A:Cross-references: FlyBase:FBgn0000043
 A:Map position: 42A
 C:Superfamily: actin
 C:Keywords: methylated amino acid
 F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 73; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 DB 164 ASSSSLEKSYELPDG 178

RESULT 5
 S05430
 actin beta - grass carp
 C:Species: Ctenopharyngodon idella (grass carp)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C:Accession: S05430
 R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.
 Nucleic Acids Res. 17, 5850, 1989
 A:Title: The beta-actin gene of carp (Ctenopharyngodon idella).
 A:Reference number: S05430; MUID:89345185; PMID:2762162
 A:Accession: S05430
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-328 <LIU>
 A:Cross-references: UNIPROT:P83751; EMBL:M25013
 C:Genetics:
 A:Introns: 41/3; 121/3; 268/1
 C:Superfamily: actin
 C:Keywords: cytoskeleton; methylated amino acid
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 73; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 DB 231 ASSSSLEKSYELPDG 245

RESULT 6
 B25819
 actin, fetal skeletal/adult cardiac muscle - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
 C:Accession: B25819
 R:Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
 J. Mol. Evol. 23, 11-22, 1986
 A:Title: Comparison of three actin-coding sequences in the mouse; evolutionary relation
 A:Reference number: A25819; MUID:86200234; PMID:3084797
 A:Accession: B25819
 A:Molecule type: mRNA
 A:Residues: 1-349 <ALO>
 A:Cross-references: UNIPROT:Q61275; GB:J00381; GB:M10652; NID:G49869; PIDN:C
 C:Superfamily: actin
 C:Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
 F:47/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 73; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 DB 205 ASSSSLEKSYELPDG 219

RESULT 7
 A26559
 actin type 5, cytosolic - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
 C:Accession: A26559
 R:Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
 Mol. Cell. Biol. 5, 1151-1162, 1985
 A:Reference number: A26559; MUID:85213487; PMID:4000121
 A:Accession: A26559
 A:Molecule type: DNA
 A:Residues: 1-362 <BER>
 C:Superfamily: actin
 C:Keywords: cytosol; methylated amino acid
 F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 73; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15

```
Db      232 ASSSSLEKSYELPDG 246
|||||
RESULT 8
A37431
actin, type 1 - Emiliana huxleyi (fragment)
C:Species: Emiliana huxleyi
C>Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: A37431
R:Bhattacharya, D.; Stickel, S.K.; Sogin, M.L.
Mol. Biol. Evol. 10, 689-703, 1993
A:Title: Isolation and molecular phylogenetic analysis of actin-coding regions from Emil
A:Reference number: A37431; MUID:93330051; PMID:7687735
A:Contents: CCM379
A:Accession: A37431
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-365 <BHA>
A:Cross-references: UNIPROT:Q41205; GB:S64188; NID:G404406; PID:G404407
A:Note: sequence extracted from NCBI backbone (NCBIN:135711, NCBIP:135712)
C:Superfamily: actin

Query Match      100.0%; Score 73; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASSSSLEKSYELPDG 15
|||||
Db      221 ASSSSLEKSYELPDG 235

RESULT 9
ATBOB
actin beta - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A39105; A02999; A14185
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P60712
A:Note: only peptides that differed in composition from the corresponding peptides of ra
R:Degeen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A:Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys
A:Reference number: A39105; MUID:84032385; PMID:6195151
A:Accession: A39105
A:Molecule type: mRNA
A:Residues: 76-227;344-374 <DEG>
A:Cross-references: GB:K00622; GB:K00623
A:Note: actins beta and gamma were not distinguished in this study
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match      100.0%; Score 73; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASSSSLEKSYELPDG 15
|||||
Db      230 ASSSSLEKSYELPDG 244

RESULT 10
ATBOG
actin beta - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A02999
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brai
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P02571
A:Note: only peptides that differed in composition from the corresponding peptides of r
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match      100.0%; Score 73; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASSSSLEKSYELPDG 15
|||||
Db      230 ASSSSLEKSYELPDG 244

RESULT 12
ATBOSM
actin, aortic smooth muscle - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C:Accession: A02997; S13480
R:Vandekerckhove, J.; Weber, K.
Differentiation 14, 123-133, 1979
A:Title: The complete amino acid sequence of actins from bovine aorta, bovine heart, bo
A:Reference number: A02997; MUID:80047657; PMID:499690
A:Accession: A02997
A:Molecule type: protein
A:Residues: 1-375 <VAN>
```

```
actin gamma - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A02999
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brai
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P02571
A:Note: only peptides that differed in composition from the corresponding peptides of r
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match      100.0%; Score 73; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASSSSLEKSYELPDG 15
|||||
Db      230 ASSSSLEKSYELPDG 244

RESULT 11
JC5818
gamma-actin - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: JC5818; PC4501
R:Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jen
Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A:Title: Actin: A target of lipopolysaccharide-induced phosphorylation in human monocyte
A:Reference number: JC5818; MUID:98096379; PMID:9434766
A:Accession: JC5818
A:Molecule type: protein
A:Residues: 1-374 <HAU>
A:Cross-references: UNIPROT:P02571
A:Experimental source: monocyte
A:Accession: PC4501
A:Molecule type: protein
A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A:Experimental source: monocyte
C:Comment: This protein is involved in a signal transduction that eventually leads to m
C:Superfamily: actin

Query Match      100.0%; Score 73; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASSSSLEKSYELPDG 15
|||||
Db      230 ASSSSLEKSYELPDG 244

RESULT 12
ATBOSM
actin, aortic smooth muscle - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C:Accession: A02997; S13480
R:Vandekerckhove, J.; Weber, K.
Differentiation 14, 123-133, 1979
A:Title: The complete amino acid sequence of actins from bovine aorta, bovine heart, bo
A:Reference number: A02997; MUID:80047657; PMID:499690
A:Accession: A02997
A:Molecule type: protein
A:Residues: 1-375 <VAN>
```

R;Zevgolis, V.G.; Sotirioudis, T.G.; Evangelopoulos, A.E.
 Biochim. Biophys. Acta 1991, 222-230, 1991
 A;Title: Phosphorylase kinase from bovine stomach smooth muscle: a Ca(2+)-dependent protein
 A;Reference number: S13480; MUID:91137633; PMID:1995080
 A;Accession: S13480
 A;Molecule type: protein
 A;Residues: 40-49 <2EV>
 A;Experimental source: stomach
 A;Note: This material appears to be actin of aortic smooth muscle type or a related molecule
 C;Superfamily: actin
 C;Keywords: acetylated amino end; methylated amino acid; muscle contraction
 F;1/Modified site: acetylated amino end (Glu) #status predicted
 F;73/Modified site: 3'-methylhistidine (His) #status experimental
 Query Match 100.0%; Score 73; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 Qy 1 ASSSLEKSYELPDG 15
 Db 231 ASSSLEKSYELPDG 245
 RESULT 13
 ATRB
 actin, skeletal muscle - rabbit
 N;Alternate names: F-actin
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-May-1999
 C;Accession: A92182; A14185; S65873; S70610; S44393; A02994
 R;Collins, J.H.; Elzinga, M.
 J. Biol. Chem. 250, 5915-5920, 1975
 A;Title: The primary structure of actin from rabbit skeletal muscle. Completion and analysis
 A;Reference number: A92182; MUID:75211334; PMID:1150665
 A;Accession: A92182
 A;Molecule type: protein
 A;Residues: 1-2,'T',4,'D',6-11,'D',13-73,'W',74-78,80-234,236-308,'T',310-375 <COL>
 A;Note: this is the final paper in a series
 A;Note: this sequence has been revised in references A14185 and A90406
 R;Vandekerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
 A;Reference number: A14185; MUID:79045349; PMID:213279
 A;Accession: A14185
 A;Molecule type: protein
 A;Residues: 1-18;69-84 <VAN>
 R;Lu, R.C.; Elzinga, M.
 Biochemistry 16, 5801-5806, 1977
 A;Title: Partial amino acid sequence of brain actin and its homology with muscle actin.
 A;Reference number: A90406; MUID:78060866; PMID:588555
 A;Contents: annotation
 A;Note: residue 235 has been added and residue 309 has been revised
 R;Vahdat, A.; Miller, C.; Phillips, M.; Muhlrud, A.; Reisler, E.
 FEBS Lett. 365, 149-151, 1995
 A;Title: A novel 27/16 kDa form of subtilisin cleaved actin: structural and functional characterization
 A;Reference number: S65873; MUID:95300963; PMID:7781768
 A;Accession: S65873
 A;Molecule type: protein
 A;Residues: 235-241 <VAN>
 R;Strzelecka-Golaszewska, H.; Wozniak, A.; Hult, T.; Lindberg, U.
 Biochem. J. 316, 713-721, 1996
 A;Title: Effects of the type of divalent cation, Ca2+ or Mg2+, bound at the high-affinity
 A;Reference number: S70610; MUID:96265033; PMID:8670143
 A;Accession: S70610
 A;Molecule type: protein
 A;Residues: 48-54;68-72;235-243 <STR>
 A;Experimental source: skeletal muscle
 R;Bertrand, R.; Derancourt, J.; Kasab, R.
 FEBS Lett. 345, 113-119, 1994
 A;Title: The covalent maleimido-benzoyl-actin-myosin head complex. Cross-linking of the
 A;Reference number: S44393; MUID:94259162; PMID:8200441
 A;Accession: S44393
 A;Molecule type: protein

A;Residues: 48-64 <BER>
 A;Experimental source: skeletal muscle
 C;Superfamily: actin
 C;Keywords: acetylated amino end; ATP binding; methylated amino acid; muscle contraction
 F;1-375/Product: actin #status experimental <MAT>
 F;1/Modified site: acetylated amino end (Asp) #status experimental
 F;73/Modified site: 3'-methylhistidine (His) #status experimental
 Query Match 100.0%; Score 73; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 Qy 1 ASSSLEKSYELPDG 15
 Db 231 ASSSLEKSYELPDG 245
 RESULT 14
 ATRC
 actin beta - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
 C;Accession: A38571; A02999
 R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
 Nucleic Acids Res. 11, 1759-1771, 1983
 A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
 A;Reference number: A38571; MUID:83168920; PMID:6300777
 A;Accession: A38571
 A;Molecule type: DNA
 A;Residues: 1-375 <NUD>
 A;Cross-references: GB:J00691; NID:G202653; PIDN:AAA0657.1; PID:G202654
 C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C;Genetics: 41/3; 121/3; 268/1; 328/3
 A;Introns: 41/3; 121/3; 268/1; 328/3
 C;Superfamily: actin
 C;Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;
 F;2-375/Product: actin beta #status predicted <MAT>
 F;73/Modified site: 3'-methylhistidine (His) #status predicted
 Query Match 100.0%; Score 73; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 Qy 1 ASSSLEKSYELPDG 15
 Db 231 ASSSLEKSYELPDG 245
 RESULT 15
 A48324
 actin beta, cytoskeletal - common carp
 C;Species: Cyprinus carpio (common carp)
 C;Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
 C;Accession: A48324
 R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
 DNA Seq. 1, 125-136, 1990
 A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
 A;Reference number: A48324; MUID:92190540; PMID:2134183
 A;Accession: A48324
 A;Molecule type: DNA
 A;Residues: 1-375 <LIU>
 A;Cross-references: UNIPROT:P83750; GB:M24113; NID:G213041; PIDN:AAA6886.1; PID:G2130/
 A;Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50,
 7 as Pro
 A;Note: the authors failed to translated the codon GGT for residue 42 as Gly
 C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C;Genetics: 41/3; 121/3; 268/3; 328/3
 A;Introns: 41/3; 121/3; 268/3; 328/3
 C;Superfamily: actin
 C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; m
 F;2-375/Product: actin beta, cytoskeletal #status predicted <MAT>
 F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
 F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 73; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASSSLEKSYELPDG 15
 |||||
 Db 231 ASSSLEKSYELPDG 245

Search completed: April 8, 2005, 10:53:08
 Job time : 10.3333 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-13
Perfect score: 73
Sequence: 1 ASSSSLEKSYELPDG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	77	2 Q6IWE2	Q6IWE2 mus musculus
2	73	100.0	89	2 Q90WZ7	Q90WZ7 poephila gu
3	73	100.0	89	2 Q90WZ9	Q90WZ9 larus argen
4	73	100.0	92	2 Q7M3Y5	Q7M3Y5 aplysia cal
5	73	100.0	93	2 Q6VQP9	Q6VQP9 romalea mic
6	73	100.0	97	2 Q6PKZ5	Q6PKZ5 oryctolagus
7	73	100.0	101	2 Q61569	Q61569 ostertergia
8	73	100.0	124	2 Q6B3W6	Q6B3W6 parastrongy
9	73	100.0	124	2 Q95319	Q95319 sus scrofa
10	73	100.0	133	2 Q96104	Q96104 apis mellif
11	73	100.0	136	2 Q95V64	Q95V64 ixodes scap
12	73	100.0	140	2 Q68U00	Q68U00 lepeophthei
13	73	100.0	141	2 Q9NAY6	Q9NAY6 papilio gla
14	73	100.0	141	2 Q6PT58	Q6PT58 squalus aca
15	73	100.0	141	2 Q6Q6W9	Q6Q6W9 ictalurus p
16	73	100.0	142	2 Q9BGH4	Q9BGH4 oryctolagus
17	73	100.0	145	2 Q6B9V8	Q6B9V8 strongyloid
18	73	100.0	146	2 Q9YI91	Q9YI91 pleocoglossu
19	73	100.0	149	2 Q8K575	Q8K575 mesocricetu
20	73	100.0	150	2 Q18549	Q18549 lytechinus
21	73	100.0	154	1 ACT4 LYTP1	Q25380 lytechinus
22	73	100.0	159	2 Q96DE1	Q96DE1 homo sapien
23	73	100.0	159	2 Q8MVL3	Q8MVL3 boltenia vi
24	73	100.0	165	2 Q96FU6	Q96FU6 homo sapien
25	73	100.0	169	2 Q8SPK6	Q8SPK6 sus scrofa
26	73	100.0	171	2 Q6GXE6	Q6GXE6 lepisosteus
27	73	100.0	171	2 Q7ZW59	Q7ZW59 rana catesb
28	73	100.0	172	1 ACT3 LYTP1	Q25379 lytechinus
29	73	100.0	181	2 Q6XJ33	Q6XJ33 drosophila
30	73	100.0	188	2 Q862P9	Q862P9 bos taurus
31	73	100.0	190	2 Q9PW57	Q9PW57 platichthys

32 73 100.0 195 2 Q9BMF8 Q9bmf8 nematostell
33 73 100.0 205 2 Q8T4J7 Q8t4j7 culicoides
34 73 100.0 207 2 Q6SQM0 Q6sqm0 cyrenoida f
35 73 100.0 207 2 Q6SQM1 Q6sqm1 cyrenoida f
36 73 100.0 211 2 Q86N81 Q86n81 sphaerichin
37 73 100.0 212 2 Q9GR83 Q9gr83 octopus vul
38 73 100.0 214 2 Q86PP6 Q86pp6 laodelphax
39 73 100.0 215 2 Q819K0 Q819k0 meloidogyne
40 73 100.0 219 2 Q93402 Q93402 carassius a
41 73 100.0 225 2 Q8QFV3 Q8qfv3 calotes ver
42 73 100.0 226 2 Q9MZW1 Q9mzw1 ovis aries
43 73 100.0 235 2 Q28937 Q28937 sus scrofa
44 73 100.0 237 2 Q9NC44 Q9nc44 sepioloidea
45 73 100.0 237 2 Q9NHN8 Q9nhn8 macrobrachi

ALIGNMENTS

RESULT 1
Q6IWE2 PRELIMINARY; PRT; 77 AA.
AC Q6IWE2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Beta-actin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SJL/JHanHsd; TISSUE=Uterus;
RA Ulrich R.G., Gerhauser I., Seeliger F., Baumgaertner W., Allidinger S.;
RT "Expression profile of matrix-metalloproteinases and their inhibitors
in acute and chronic demyelinating Theiler's murine
encephalomyelitis.";
RL Acta Neuropathol. 108:366-366(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SJL/JHanHsd; TISSUE=Uterus;
RA Ulrich R.G., Gerhauser I., Allidinger S., Baumgaertner W.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY618569; AAT40730.1; -
FT NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 8594 MW; 5F59DFF1137A368C CRC64;
Query Match 100.0%; Score 73; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASSSSLEKSYELPDG 15
|||
Db 35 ASSSSLEKSYELPDG 49
RESULT 2
Q90WZ7 PRELIMINARY; PRT; 89 AA.
AC Q90WZ7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Poephila guttata (Zebra finch) (Taeniopygia guttata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
OC Estrildinae; Taeniopygia.
RN NCBI_TaxID=59729;
RN [1]
RP SEQUENCE FROM N.A.

```

RX MEDLINE=21572031; PubMed=11714249; DOI=10.1006/taap.2001.9273;
RA Lorenzen A., Casley W.L., Moon T.W.;
RT "A reverse transcription-polymerase chain reaction bioassay for avian
RT vitellogenin mRNA."
RL Toxicol. Appl. Pharmacol. 176:169-180 (2001).
DR EMBL; AY045726; AAL01534.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10074 MW; 3DDF4FAC4747EFB2 CRC64;

Query Match 100.0%; Score 73; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
Db 25 ASSSSLEKSYELPDG 39

RESULT 3
Q90WZ9 PRELIMINARY; PRT; 89 AA.
AC Q90WZ9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Larus argentatus (Herring gull).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Charadriiformes; Laridae; Larus.
OX NCBI_TaxID=35669;
[1]
SEQUENCE FROM N.A.
MEDLINE=21572031; PubMed=11714249; DOI=10.1006/taap.2001.9273;
RA Lorenzen A., Casley W.L., Moon T.W.;
RT "A reverse transcription-polymerase chain reaction bioassay for avian
RT vitellogenin mRNA."
RL Toxicol. Appl. Pharmacol. 176:169-180 (2001).
DR EMBL; AY045724; AAL01532.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10074 MW; 3DDF4FAC4747EFB2 CRC64;

Query Match 100.0%; Score 73; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
Db 25 ASSSSLEKSYELPDG 39

RESULT 4
Q7M3Y5 PRELIMINARY; PRT; 92 AA.
AC Q7M3Y5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Actin (Fragments).
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;

[1]
SEQUENCE.
MEDLINE=88320566; PubMed=3413132;
RA Kennedy T.E., Gawinowicz M.A., Barzilai A., Kandel E.R., Sweatt J.D.;
RT "Sequencing of proteins from two-dimensional gels by using in situ
RT digestion and transfer of peptides to polyvinylidene difluoride
RT membranes: application to proteins associated with sensitization in
RT Aplysia."
RL Proc. Natl. Acad. Sci. U.S.A. 85:7008-7012 (1988).
[2]
SEQUENCE.
MEDLINE=89276264; PubMed=2731514;
RA Sweatt J.D., Kennedy T.E., Wager-Smith K., Gawinowicz M.A.,
RA Barzilai A., Karl K.A., Kandel E.R.;
RT "Development of a database of amino acid sequences for proteins
RT identified and isolated on two-dimensional polyacrylamide gels."
RL Electrophoresis 10:152-157 (1989).
DR PIR; A31409; A31409.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
FT NON_TER 1
FT NON_TER 92
SQ SEQUENCE 92 AA; 9513 MW; 3C36BEFE381A701C CRC64;

Query Match 100.0%; Score 73; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
Db 60 ASSSSLEKSYELPDG 74

RESULT 5
Q6VQP9 PRELIMINARY; PRT; 93 AA.
AC Q6VQP9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin (Fragment).
OS Romalea microptera (rubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
[1]
SEQUENCE FROM N.A.
Fei H., Martin T., Jaskowiack K., Hatle J., Borst D.W.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY331667; AAQ24502.1; -.
FT NON_TER 1
FT NON_TER 93
SQ SEQUENCE 93 AA; 10698 MW; 5635F5335A532256 CRC64;

Query Match 100.0%; Score 73; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
Db 73 ASSSSLEKSYELPDG 87

RESULT 6
Q6PKZ5 PRELIMINARY; PRT; 97 AA.
AC Q6PKZ5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytoplasmic beta-actin (Fragment).
OC Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Enns P.J., Surtel D.A., Frings E.J., Bulstra S.K., Kuijter R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Enns P.J., Surtel D.A., Reilly K., Bulstra S.K., Kuijter R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY598932; AAT02354.1; -
 FT NON_TER 1
 FT NON_TER 97
 SQ SEQUENCE 97 AA; 11019 MW; CFDC2B52E0903997 CRC64;

Query Match 100.0%; Score 73; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 |||||
 DB 72 ASSSSLEKSYELPDG 86

RESULT 7

ID O61569 PRELIMINARY; PRT; 101 AA.
 AC O61569;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Actin (Fragment).
 GN Name=act;
 OS Ostertagia ostertagi.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
 OX NCBI_TaxID=6317;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20233682; PubMed=10769181; DOI=10.1042/0264-6021:3470763;
 RA Moore J.; Tetley L.; Devaney E.;
 RT "Identification of abundant mRNAs from the third stage larvae of the
 RL parasitic nematode, Ostertagia ostertagi."
 RL Biochem. J. 347:763-770(2000).
 DR EMBL: AF052043; AAC06292.1; -
 DR HSP: P10983; I04X.
 DR GO: GO:0015629; C:actin cytoskeleton; IEA.
 DR GO: GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro: IPR004000; Actin_like.
 DR Pfam: PF00022; Actin; 1.
 FT NON_TER 1
 FT NON_TER 101
 SQ SEQUENCE 101 AA; 11499 MW; 7AF3A21892AD0D75 CRC64;

Query Match 100.0%; Score 73; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 |||||
 DB 68 ASSSSLEKSYELPDG 82

RESULT 8

ID Q6B9W6 PRELIMINARY; PRT; 124 AA.
 AC Q6B9W6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE ACT-3 (fragment).
 OS Parastromyloides trichosuri.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

OC Panagrolaimoidea; Strongyloidea; Parastromyloidea.
 OX NCBI_TaxID=131310;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crook M., Thompson F.J., Grant W.N., Viney M.E.;
 RT "daf-7 and the development of Strongyloides ratti and
 RL Parastromyloides trichosuri."
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY672703; AAT79342.1; -
 DR InterPro: IPR004000; Actin_like.
 DR Pfam: PF00022; Actin; 1.
 FT NON_TER 1
 FT NON_TER 124
 SQ SEQUENCE 124 AA; 13776 MW; 699F9C1639807BDC CRC64;

Query Match 100.0%; Score 73; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 |||||
 DB 28 ASSSSLEKSYELPDG 42

RESULT 9

ID Q95319 PRELIMINARY; PRT; 124 AA.
 AC Q95319;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-actin, cytoplasmic (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z81198; CAB03563.1; -
 DR HSP: P60712; IHLU.
 DR GO: GO:0015629; C:actin cytoskeleton; IEA.
 DR GO: GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro: IPR004000; Actin_like.
 DR Pfam: PF00022; Actin; 1.
 FT NON_TER 1
 FT NON_TER 124
 SQ SEQUENCE 124 AA; 13860 MW; CB61B9AA97A9AF49 CRC64;

Query Match 100.0%; Score 73; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 |||||
 DB 26 ASSSSLEKSYELPDG 40

RESULT 10

ID O96104 PRELIMINARY; PRT; 133 AA.
 AC O96104;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Actin (Fragment).
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 OX NCBI_TaxID=7460;


```
AC Q6PT58;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-actin (Fragment).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosqualea; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.
RA Klovins J., Haitina T., Ringholm A., Lowgren M., Fridmanis D.,
RA Slaidina M., Schioth H.B.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY581300; AAS90345.1; -
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR SMART; SM00268; ACTIN; 1.
DR KW Structural protein.
FT NON_TER 1
FT NON_TER 141
FT NON_TER 141
SQ SEQUENCE 141 AA; 15632 MW; 5DC92A9C4FC3CBDA CRC64;

Query Match 100.0%; Score 73; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
Db 16 ASSSSLEKSYELPDG 30

RESULT 15
Q6Q6W9 PRELIMINARY; PRT; 141 AA.
AC Q6Q6W9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-actin (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Trant J.M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY555575; AAS66998.1; -
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR SMART; SM00268; ACTIN; 1.
DR KW Structural protein.
FT NON_TER 1
FT NON_TER 141
FT NON_TER 141
SQ SEQUENCE 141 AA; 15750 MW; 710591BB45A234A8 CRC64;

Query Match 100.0%; Score 73; DB 2; Length 141;
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Best Local Similarity 100.0%; Pred. No. 9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
Db 10 ASSSSLEKSYELPDG 24

Search completed: April 8, 2005, 12:03:14
Job time : 58.8667 secs
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-14

Perfect score: 75

Sequence: 1 APSTWKIKIAPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Genesecp1980s:*

2: Genesecp1990s:*

3: Genesecp2000s:*

4: Genesecp2001s:*

5: Genesecp2002s:*

6: Genesecp2003as:*

7: Genesecp2003bs:*

8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	15	2 AAW92540	Beta-acti
2	75	100.0	86	4 ABG08617	Novel hum
3	75	100.0	100	4 AAM81404	Human hae
4	75	100.0	100	4 AAM81907	Human hae
5	75	100.0	101	3 AAB57154	Human pro
6	75	100.0	110	5 ABP42928	Human ova
7	75	100.0	145	5 ABP43127	Human ova
8	75	100.0	147	4 AAM80875	Human hae
9	75	100.0	147	4 AAM81886	Human hae
10	75	100.0	147	4 AAM81332	Human hae
11	75	100.0	149	8 ABO84771	Human can
12	75	100.0	181	4 ABG11441	Novel hum
13	75	100.0	274	6 ABU70549	Human adi
14	75	100.0	294	7 ADI63068	Human apo
15	75	100.0	297	4 ABG15100	Novel hum
16	75	100.0	332	7 ADI63011	Human apo
17	75	100.0	334	6 ABP98860	Human str
18	75	100.0	342	7 ADM05323	Human pro
19	75	100.0	374	3 AAY78101	Misgurnus
20	75	100.0	374	3 AAB12985	Human bet
21	75	100.0	375	1 AAP61532	Sequence
22	75	100.0	375	2 AAR50328	Drug resi
23	75	100.0	375	3 AAB15017	Posttrans
24	75	100.0	375	3 AAY94569	Human car
25	75	100.0	375	3 AAB15016	Posttrans

ALIGNMENTS

RESULT 1				
AAW92540				
ID	AAW92540	standard; peptide; 15 AA.		
XX	AC	AAW92540;		
XX	AC			
DT	26-APR-1999	(first entry)		
XX				
DE	Beta-actin reference peptide substrate #14.			
XX				
KW	Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin;			
KW	tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity.			
XX				
OS	Synthetic.			
XX				
PN	WO9853322-A1.			
XX				
PD	26-NOV-1998.			
XX				
PF	22-MAY-1998;	98WO-GB001485.		
XX				
PR	23-MAY-1997;	97GB-00010762.		
XX				
PA	(CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.			
XX				
PI	Willison K, Hynes G, Liou AK;			
XX				
DR	WPI; 1999-070162/06.			
XX				
PT	Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.			
XX				
PS	Disclosure; Fig 10; 97pp; English.			
XX				
CC	This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding			

Abb77395 Human act
Abm64271 Angiogene
Abm04830 Rat cytop
Adb85212 Rat actin
Ade61174 Rat Prote
Adf30525 Rat angio
Adi63062 Human apo
Adi62970 Human apo
Adi63040 Human apo
Adl13002 Human ste
Adj78489 Actin pro
Adl14103 Human sar
Adp12391 Protein e
Adq26098 Gamma 1 a
Abo84772 Human can
Abm80841 Tumour-as
Adn23274 Bacterial
Adm88828 Amino aci
Adm88825 Amino aci
Adm88826 Amino aci

75 100.0 375 5 ABB77395
75 100.0 375 6 ABR64271
75 100.0 375 6 ABM04830
75 100.0 375 7 ADS85212
75 100.0 375 7 ADE61174
75 100.0 375 7 ADF30525
75 100.0 375 7 ADI63062
75 100.0 375 7 ADI62970
75 100.0 375 7 ADI63040
75 100.0 375 7 ADL13002
75 100.0 375 8 ADJ78489
75 100.0 375 8 ADL14103
75 100.0 375 8 ADP12391
75 100.0 375 8 ADQ26098
75 100.0 375 8 ABO84772
75 100.0 375 8 ABM80841
75 100.0 375 8 ADN23274
75 100.0 375 8 ADM88828
75 100.0 375 8 ADM88825
75 100.0 375 8 ADM88826

CC agents may target cells that are actively synthesising tubulin etc.
CC (unlike known microtubule-stabilising agents that affect all cells), so
CC should have reduced toxicity for normal cells. AAM92527-W92541 are
CC peptide substrates used in the method of the invention
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 75; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. NO. 8.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APSTWKIKIAPP 15
DB 1 APSTWKIKIAPP 15
RESULT 2
ABG08617
ID ABG08617 standard; protein; 86 AA.
XX
AC ABG08617;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #8608.
XX
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS72804.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 38976; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 86 AA;
Query Match 100.0%; Score 75; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. NO. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APSTWKIKIAPP 15
DB 32 APSTWKIKIAPP 46
RESULT 3
AAM81404
ID AAM81404 standard; protein; 100 AA.
XX
AC AAM81404;
XX
DT 13-NOV-2001 (first entry)
XX
DE Human haematological malignancy-related antigen #1102.
XX
DE Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
XX
OS Homo sapiens.
XX
PN WO200164886-A2.
XX
PD 07-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US007272.
XX
PR 01-MAR-2000; 2000US-0186126P.
PR 17-MAR-2000; 2000US-0190479P.
PR 27-APR-2000; 2000US-0200545P.
PR 28-APR-2000; 2000US-0200303P.
PR 28-APR-2000; 2000US-0200779P.
PR 01-MAY-2000; 2000US-0200999P.
PR 04-MAY-2000; 2000US-0202084P.
PR 22-MAY-2000; 2000US-0206201P.
PR 14-JUL-2000; 2000US-0218950P.
PR 03-AUG-2000; 2000US-0222903P.
PR 04-AUG-2000; 2000US-0223418P.
PR 07-AUG-2000; 2000US-0223378P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J;
XX
XX WPI; 2001-514842/56.
XX
CC Compositions and methods for the detection of hematological malignancies,
CC e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
CC Hodgkin's and T/B cell non-Hodgkin's lymphoma.
XX
PS Claim 1; Page 953; 1252pp; English.
XX
CC The present invention relates to compositions and methods for the
CC detection, diagnosis and therapy of haematological malignancies. The
CC present sequence is the protein sequence of a human haematological
CC malignancy related antigen. The methods of the present invention comprise
CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma
XX

SQ Sequence 100 AA;
 Query Match 100.0%; Score 75; DB 4; Length 100;
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTWKIKIAPP 15
 DB 66 APSTWKIKIAPP 80
 |||||

RESULT 4
 AAM81907
 ID AAM81907 standard; protein; 100 AA.
 AC AAM81907;
 XX
 XX
 DT 13-NOV-2001 (first entry)
 XX
 XX Human haematological malignancy-related antigen #1605.
 XX
 KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX
 OS Homo sapiens.
 XX
 XX WO200164886-A2.
 PN
 PD
 PD 07-SEP-2001.
 XX
 XX 01-MAR-2001; 2001WO-US007272.
 XX
 PR 01-MAR-2000; 2000US-0186126P.
 PR 17-MAR-2000; 2000US-0190479P.
 PR 27-APR-2000; 2000US-0200545P.
 PR 28-APR-2000; 2000US-0200303P.
 PR 28-APR-2000; 2000US-0200779P.
 PR 01-MAY-2000; 2000US-0200999P.
 PR 04-MAY-2000; 2000US-0202084P.
 PR 22-MAY-2000; 2000US-0206201P.
 PR 14-JUL-2000; 2000US-0218950P.
 PR 03-AUG-2000; 2000US-0222303P.
 PR 04-AUG-2000; 2000US-0223416P.
 PR 07-AUG-2000; 2000US-0223378P.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Gaiger A, Algate PA, Mannion J;
 XX
 XX WPI; 2001-514842/56.
 XX
 XX Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX
 XX Claim 1; Page 1149-1150; 1252pp; English.
 XX
 CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma
 XX
 XX SQ Sequence 100 AA;
 Query Match 100.0%; Score 75; DB 4; Length 100;

Best Local Similarity 100.0%; Pred. No. 6.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTWKIKIAPP 15
 DB 66 APSTWKIKIAPP 80
 |||||

RESULT 5
 AAB57154
 ID AAB57154 standard; protein; 101 AA.
 AC AAB57154;
 XX
 XX
 DT 13-MAR-2001 (first entry)
 XX
 XX Human prostate cancer antigen protein sequence SEQ ID NO:1732.
 XX
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW urological; gastrointestinal; nephrotropic; antineoplastic; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.
 XX
 OS Homo sapiens.
 XX
 XX WO2000055174-A1.
 PN
 PD 21-SEP-2000.
 XX
 XX 08-MAR-2000; 2000WO-US005988.
 XX
 XX 12-MAR-1999; 99US-0124270P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (ROSE/) ROSEN C A.
 XX
 XX Rosen CA, Ruben SM;
 XX
 XX WPI; 2000-587513/55.
 DR N-PSDB; AAF16357.
 XX
 PT Prostate cancer associated gene sequences, referred to as prostate cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as prostate cancer.
 XX
 XX Claim 1; Page 2204; 2338pp; English.
 XX
 CC AAF15566 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, urological, gastrointestinal,
 CC nephrotropic, antineoplastic, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention
 XX
 XX SQ Sequence 101 AA;
 Query Match 100.0%; Score 75; DB 3; Length 101;
 Best Local Similarity 100.0%; Pred. No. 6.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTWKIKIAPP 15
 DB 35 APSTWKIKIAPP 49
 |||||

CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 110 AA;
 Query Match 100.0%; Score 75; DB 5; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 APSTMKIKIIPPER 15
 Db 56 APSTMKIKIIPPER 70
 RESULT 7
 ABP43127
 ID ABP43127 standard; protein; 145 AA.
 AC ABP43127;
 XX 22-AUG-2002 (first entry)
 DT 22-AUG-2002 (first entry)
 XX Human ovarian antigen HVBD91, SEQ ID NO:4259.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX Homo sapiens.
 OS
 XX
 XX WO200200677-A1.
 PN
 XX
 XX 03-JAN-2002.
 PD
 XX 07-JUN-2001; 2001WO-US018569.
 PF
 XX 07-JUN-2000; 2000US-0209467P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Birse CE, Rosen CA;
 PI
 XX WPI; 2002-147878/19.
 DR
 XX N-PSDB; ABQ56005.

Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 cancer), immune disorders, cardiovascular disorders and neurological
 diseases.
 Claim 11; SEQ ID NO 4060; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-
 ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 encompasses polypeptides 90% identical and polynucleotides 95% identical
 to the sequences of the invention. The invention additionally relates to
 recombinant vectors and host cells comprising human ovarian antigen
 polynucleotides, antibodies against human ovarian antigens, and the use
 of ovarian antigen polynucleotides and polypeptides in diagnosing,
 treating, prognosing or preventing various ovary and/or breast-related
 disorders. Such conditions include ovarian cancer and breast cancer, and
 metastatic tumours of ovarian or breast origin, reproductive system
 disorders (e.g., infertility, disorders of pregnancy, anovulation,
 polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 vaginitis), immune disorders (e.g., congenital and acquired
 immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 blood-related disorders (e.g., anaemia), cardiovascular disorders,
 respiratory disorders, neurological disorders, gastrointestinal disorders
 and urinary system disorders. Ovarian antigen polypeptides and
 polynucleotides may also be used in screening for compounds which
 modulate ovarian antigen expression or activity. The polynucleotides may
 further be used for gene therapy, chromosome mapping, in the
 identification of individuals and in forensic analysis, and the
 polypeptides may be used as food additives or to prepare antibodies
 useful in disease diagnosis, drug targeting and phenotyping. The present
 sequence represents a human ovarian antigen of the invention. Note: The

RESULT 6
 ABP42928
 ID ABP42928 standard; protein; 110 AA.
 AC ABP42928;
 XX 22-AUG-2002 (first entry)
 DT 22-AUG-2002 (first entry)
 XX Human ovarian antigen HPRS46, SEQ ID NO:4060.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX Homo sapiens.
 OS
 XX
 XX WO200200677-A1.
 PN
 XX
 XX 03-JAN-2002.
 PD
 XX 07-JUN-2001; 2001WO-US018569.
 PF
 XX 07-JUN-2000; 2000US-0209467P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Birse CE, Rosen CA;
 PI
 XX WPI; 2002-147878/19.
 DR
 XX N-PSDB; ABQ56005.

Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 cancer), immune disorders, cardiovascular disorders and neurological
 diseases.
 Claim 11; SEQ ID NO 4060; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-
 ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 encompasses polypeptides 90% identical and polynucleotides 95% identical
 to the sequences of the invention. The invention additionally relates to
 recombinant vectors and host cells comprising human ovarian antigen
 polynucleotides, antibodies against human ovarian antigens, and the use
 of ovarian antigen polynucleotides and polypeptides in diagnosing,
 treating, prognosing or preventing various ovary and/or breast-related
 disorders. Such conditions include ovarian cancer and breast cancer, and
 metastatic tumours of ovarian or breast origin, reproductive system
 disorders (e.g., infertility, disorders of pregnancy, anovulation,
 polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 vaginitis), immune disorders (e.g., congenital and acquired
 immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 blood-related disorders (e.g., anaemia), cardiovascular disorders,
 respiratory disorders, neurological disorders, gastrointestinal disorders
 and urinary system disorders. Ovarian antigen polypeptides and
 polynucleotides may also be used in screening for compounds which
 modulate ovarian antigen expression or activity. The polynucleotides may
 further be used for gene therapy, chromosome mapping, in the
 identification of individuals and in forensic analysis, and the
 polypeptides may be used as food additives or to prepare antibodies
 useful in disease diagnosis, drug targeting and phenotyping. The present
 sequence represents a human ovarian antigen of the invention. Note: The

CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 145 AA;
 Query Match 100.0%; Score 75; DB 5; Length 145;
 Best Local Similarity 100.0%; Pred. No. 9.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
 DB 91 APSTMKIKIAPP 105

RESULT 8
 AAM80875
 ID AAM80875 standard; protein; 147 AA.

AC AAM80875;

DT 13-NOV-2001 (first entry)

DE Human haematological malignancy-related antigen #573.

KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;

KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

OS Homo sapiens.

PN WO200164886-A2.

PD 07-SEP-2001.

PF 01-MAR-2001; 2001WO-US007272.

PR 01-MAR-2000; 2000US-0186126P.

PR 17-MAR-2000; 2000US-0190479P.

PR 27-APR-2000; 2000US-0200545P.

PR 28-APR-2000; 2000US-0200303P.

PR 28-APR-2000; 2000US-0200779P.

PR 01-MAY-2000; 2000US-0200999P.

PR 04-MAY-2000; 2000US-0202084P.

PR 22-MAY-2000; 2000US-0206201P.

PR 14-JUL-2000; 2000US-0218950P.

PR 03-AUG-2000; 2000US-0222903P.

PR 04-AUG-2000; 2000US-0223416P.

PR 07-AUG-2000; 2000US-0223378P.

PA (CORI-) CORIXA CORP.

PI Gaiger A, Algate PA, Mannion J;

PT WPI; 2001-514842/56.

XX Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.

PS Claim 1; Page 743-744; 1252pp; English.
 XX The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma

XX Sequence 147 AA;

SQ Query Match 100.0%; Score 75; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
 DB 93 APSTMKIKIAPP 107

RESULT 9
 AAM81886
 ID AAM81886 standard; protein; 147 AA.

AC AAM81886;

DT 13-NOV-2001 (first entry)

DE Human haematological malignancy-related antigen #1584.

KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;

KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

OS Homo sapiens.

PN WO200164886-A2.

PD 07-SEP-2001.

PF 01-MAR-2001; 2001WO-US007272.

PR 01-MAR-2000; 2000US-0186126P.

PR 17-MAR-2000; 2000US-0190479P.

PR 27-APR-2000; 2000US-0200545P.

PR 28-APR-2000; 2000US-0200303P.

PR 28-APR-2000; 2000US-0200779P.

PR 01-MAY-2000; 2000US-0200999P.

PR 04-MAY-2000; 2000US-0202084P.

PR 22-MAY-2000; 2000US-0206201P.

PR 14-JUL-2000; 2000US-0218950P.

PR 03-AUG-2000; 2000US-0222903P.

PR 04-AUG-2000; 2000US-0223416P.

PR 07-AUG-2000; 2000US-0223378P.

PA (CORI-) CORIXA CORP.

PI Gaiger A, Algate PA, Mannion J;

PT WPI; 2001-514842/56.

XX Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.

PS Claim 1; Page 1141; 1252pp; English.

XX The present invention relates to compositions and methods for the

CC detection, diagnosis and therapy of haematological malignancies. The
CC present sequence is the protein sequence of a human haematological
CC malignancy related antigen. The methods of the present invention comprise
CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma
XX Sequence 147 AA;
SQ

Query Match 100.0%; Score 75; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APSTMKIKIAPP 15
DB 93 APSTMKIKIAPP 107

RESULT 10
AAM81332
ID AAM81332 standard; protein; 147 AA.
XX AC AAM81332;
XX DE 13-NOV-2001 (first entry)
XX DE Human haematological malignancy-related antigen #1030.
XX KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
XX OS Homo sapiens.
XX WO200164886-A2.
XX PN 07-SEP-2001.
XX PD 01-MAR-2001; 2001WO-US007272.
XX PF 01-MAR-2000; 2000US-0186128P.
XX PR 17-MAR-2000; 2000US-0190479P.
XX PR 27-APR-2000; 2000US-0200545P.
XX PR 28-APR-2000; 2000US-0200303P.
XX PR 28-APR-2000; 2000US-0200779P.
XX PR 01-MAY-2000; 2000US-0200999P.
XX PR 04-MAY-2000; 2000US-0202084P.
XX PR 22-MAY-2000; 2000US-0206201P.
XX PR 14-JUL-2000; 2000US-0218950P.
XX PR 03-AUG-2000; 2000US-0222903P.
XX PR 04-AUG-2000; 2000US-0223416P.
XX PR 07-AUG-2000; 2000US-0223378P.
XX PA (CORI-) CORIXA CORP.
XX PI Gaiger A, Algate PA, Mannion J;
XX WPI; 2001-514842/56.
XX DR Compositions and methods for the detection of hematological malignancies,
XX e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
XX Hodgkin's and T/B cell non-Hodgkin's lymphoma.
XX PS Claim 1; Page 925; 1252pp; English.
XX CC The present invention relates to compositions and methods for the
CC detection, diagnosis and therapy of haematological malignancies. The
CC present sequence is the protein sequence of a human haematological
CC malignancy related antigen. The methods of the present invention comprise

CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma
XX Sequence 147 AA;
SQ

Query Match 100.0%; Score 75; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APSTMKIKIAPP 15
DB 93 APSTMKIKIAPP 107

RESULT 11
ABO84771
ID ABO84771 standard; protein; 149 AA.
XX AC ABO84771;
XX DT 18-NOV-2004 (first entry)
XX DE Human cancer-associated protein (CAP) HP07-010.
XX KW Human; cancer-associated protein; CAP; cancer; cytostatic.
XX OS Homo sapiens.
XX WO2004058146-A2.
XX PD 15-JUL-2004.
XX PF 15-DEC-2003; 2003WO-US040081.
XX PR 17-DEC-2002; 2002US-00322281.
XX PA (SAGR-) SAGRES DISCOVERY INC.
XX PI Morris DW, Malandro MS;
XX WPI; 2004-499109/47.
XX N-PSDB; ABD33111.
XX Novel human cancer associated protein encoded within open reading frame
XX of cancer associated gene, useful as targets for diagnosing cancer.

Claim 18; SEQ ID NO 66; 182pp; English.
The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CAP of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 100.0%; Score 75; DB 8; Length 149;
SQ Sequence 149 AA;

Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
DB 95 APSTMKIKIAPP 109

RESULT 12
ABG11441
ID ABG11441 standard; protein; 181 AA.
XX
AC ABG11441;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #11432.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS75628.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 41800; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 181 AA;

Query Match 100.0%; Score 75; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
DB 127 APSTMKIKIAPP 141

RESULT 13
ABU70549
ID ABU70549 standard; protein; 274 AA.
XX
AC ABU70549;
XX
DT 10-JUN-2003 (first entry)
XX
DE Human adipocyte Selected Interacting domain, SID, #180.
XX
KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;
KW antidiabetic; protein-protein interaction; diabetes;
KW yeast 2-hybrid assay; metabolic disorder; obesity.
XX
OS Homo sapiens.
XX
PN WO200286122-A2.
XX
PD 31-OCT-2002.
XX
PF 14-MAR-2002; 2002WO-BP003768.
XX
PR 14-MAR-2001; 2001US-0275734P.
XX
PA (HYBR-) HYBRIGENICS.
XX
PI Legrain P, Daviet L;
XX
DR WPI; 2003-103412/09.
DR N-PSDB; ACA57093.
XX
PT New complex between two interacting proteins in adipocyte cells, useful
PT for identifying selected interacting domains that modulate protein
PT interactions, or for preventing or treating metabolic disorders such as
PT obesity or diabetes.
XX
PS Claim 6; Page 167; 382pp; English.
XX
CC The invention relates to a complex between two interacting proteins in
CC adipocyte cells, given in the specification. The proteins are identified
CC by selecting a bait protein from a known adipocyte marker and then
CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
CC members of an adipocyte cDNA library. The proteins are designated SID
CC (RTM) (selected interacting domains) proteins. Also included are a
CC polynucleotide encoding a polypeptide in the adipocyte cells, a
CC recombinant host cell expressing at least one of the interacting
CC polypeptides of the complex, selecting a modulating compound in adipocyte
CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
CC sequences given in the specification (including its fragment or variant),
CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
CC given in the specification (including its fragment or variant), a vector
CC comprising the SID (RTM) polynucleotide, a recombinant host cell
CC comprising the vector, a protein chip comprising the polypeptides and a
CC record comprising all or part of the data, listed in the specification.
CC The complex, polypeptides, polynucleotides and compounds are useful for
CC preventing or treating metabolic disorders such as obesity or diabetes.
CC The polynucleotides are useful as probes or primers. The complex is
CC particularly useful for identifying selected interacting domains (SID
CC (RTM)) for screening drugs that modulate the protein interaction, thus
CC exhibiting the therapeutic effect. The present sequence represents a SID
CC (prey) protein of the invention
XX
SQ Sequence 274 AA;

Query Match 100.0%; Score 75; DB 6; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTWKIKIAPP 15
| | | | | | | | | | | | | | | |
Db 240 APSTWKIKIAPP 254

RESULT 15
AEG15100
ID ABG15100 standard; protein; 297 AA.
XX
AC ABG15100;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #15091.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS79287.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 45459; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 297 AA;

Query Match 100.0%; Score 75; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTWKIKIAPP 15
| | | | | | | | | | | | | | | |
Db 220 APSTWKIKIAPP 234

RESULT 14
ADI63068
ID ADI63068 standard; protein; 294 AA.
XX
AC ADI63068;
XX
DT 22-APR-2004 (first entry)
XX
DE Human apoptosis-associated protein SEQ ID 511.
XX
KW apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
KW antiinflammatory; antiarthritic; dermatological; antiinflammatory;
KW hepatotropic; virucide; neurotropic; anticonvulsant; antiparkinsonian;
KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;
KW autoimmune disease; degenerative disease; viral infection; leukaemia;
KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
KW lupus; hepatitis; influenza viruses; Alzheimer's disease;
KW Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
KW alcoholic liver disease; human.
XX
OS Homo sapiens.
XX
PN WO2003058021-A2.
XX
PD 17-JUL-2003.
XX
PF 13-JAN-2003; 2003WO-EF000270.
XX
PR 11-JAN-2002; 2002DE-01000856.
XX
PA (XANT-) XANTOS BIOMEDICINE AG.
XX
PI Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;
XX
DR WPI; 2003-542134/51.

New nucleic acids involved in apoptosis, useful for diagnosis and
treatment of e.g. tumors and degenerative disease, also related proteins,
antibodies and modulators.

Claim 1b; SEQ ID NO 511; 517pp; German.

This invention describes novel nucleic acid molecules that are associated
with apoptosis and encode a polypeptide and are derived from a normalised
gene library (embryonic or liver) or clone collections, and the extent of
apoptosis measured by cell death detection assay or the CPRG assay
(measuring loss of membrane integrity). The products of the invention
have cytostatic, neuroprotective, immunosuppressive, antirheumatic,
antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,
neurotropic, anticonvulsant, antiparkinsonian, vasotropic,
cerebroprotective and antialcoholic activity and can be used for gene
therapy. The polynucleotides also related vectors, hosts (or their
extracts), encoded polypeptide (or their receptors) and/or agents that
inhibit their activity (including antisense sequences) are used for
treatment or prevention of tumours, autoimmune or degenerative diseases
and viral infections, specifically leukaemia, carcinoma, sarcoma,
multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection
with hepatitis or influenza viruses, Alzheimer's, Huntington's or
Parkinson's diseases, reperfusion injury, stroke and alcoholic liver
disease. Detection of the polynucleotides and derived polypeptides can
also be used for diagnosis of these diseases. This sequence represents an
apoptosis-associated protein described in the invention.

Sequence 294 AA;

Query Match 100.0%; Score 75; DB 7; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.0002;

Qy 1 APSTMKIKIIPPER 15
| | | | | | | | | |
Db 274 APSTMKIKIIPPER 288

Search completed: April 8, 2005, 10:50:50
Job time : 63.4 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-14
Sequence: 1 APSTWKIKIAPP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pdp.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pdp.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pdp.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pdp.*
- 5: /cgn2_6/prodata/1/iaa/PTUS COMB.pdp.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	239	4	US-09-949-016-10409 Sequence 10409, A
2	75	100.0	374	3	US-08-609-236-6 Sequence 6, Appli
3	75	100.0	374	3	US-09-306-446C-2 Sequence 2, Appli
4	75	100.0	375	3	US-09-106-217-16 Sequence 16, Appl
5	75	100.0	375	4	US-09-976-594-731 Sequence 731, App
6	75	100.0	376	1	US-08-588-113-2 Sequence 2, Appli
7	75	100.0	376	4	US-09-949-016-6100 Sequence 6100, Ap
8	75	100.0	377	3	US-09-106-217-2 Sequence 2, Appli
9	75	100.0	377	4	US-09-919-172-33 Sequence 33, Appl
10	75	100.0	377	4	US-09-917-254-53 Sequence 53, Appl
11	75	100.0	386	4	US-09-949-016-7721 Sequence 7721, Ap
12	75	100.0	399	4	US-09-949-016-9424 Sequence 9424, Ap
13	75	100.0	402	4	US-09-949-016-10757 Sequence 10757, A
14	75	100.0	404	4	US-09-949-016-11313 Sequence 11313, A
15	70	93.3	375	3	US-09-171-337A-7 Sequence 7, Appli
16	70	93.3	375	4	US-09-631-022-7 Sequence 7, Appli
17	70	93.3	377	4	US-09-248-796A-14109 Sequence 14109, A
18	69	92.0	375	2	US-08-494-151-14 Sequence 14, Appl
19	62	82.7	375	3	US-09-171-337A-8 Sequence 8, Appli
20	62	82.7	375	4	US-09-631-022-8 Sequence 8, Appli
21	56	74.7	30	4	US-09-270-767-38151 Sequence 38151, A
22	56	74.7	30	4	US-09-270-767-53368 Sequence 53368, A
23	49	65.3	336	4	US-09-248-796A-14108 Sequence 14108, A
24	47	62.7	376	4	US-09-538-092-1110 Sequence 1110, Ap
25	47	62.7	376	4	US-09-949-016-6656 Sequence 6656, Ap
26	47	62.7	376	4	US-09-949-016-8452 Sequence 8452, Ap
27	46	61.3	384	4	US-09-538-092-395 Sequence 395, App

28	46	61.3	535	4	US-09-902-540-10002 Sequence 10002, A
29	44	58.7	362	4	US-09-949-016-7725 Sequence 7725, Ap
30	44	58.7	376	4	US-09-538-092-1109 Sequence 1109, Ap
31	44	58.7	437	4	US-09-107-532A-6709 Sequence 6709, Ap
32	41	54.7	248	4	US-09-328-352-6421 Sequence 6421, Ap
33	40	53.3	385	4	US-09-902-540-14731 Sequence 14731, A
34	40	53.3	403	4	US-09-270-767-37943 Sequence 37943, A
35	40	53.3	403	4	US-09-270-767-53160 Sequence 53160, A
36	40	53.3	469	4	US-09-902-540-12213 Sequence 12213, A
37	39	52.0	60	3	US-09-306-446C-6 Sequence 6, Appli
38	39	52.0	176	4	US-09-252-991A-16997 Sequence 16997, A
39	38	50.7	154	4	US-09-587-789-13 Sequence 13, Appl
40	38	50.7	162	4	US-09-270-767-36157 Sequence 36157, A
41	38	50.7	162	4	US-09-270-767-51374 Sequence 51374, A
42	38	50.7	183	3	US-08-483-534A-7 Sequence 7, Appli
43	38	50.7	310	1	US-08-129-456A-37 Sequence 37, Appl
44	38	50.7	312	4	US-08-360-821B-36 Sequence 36, Appl
45	38	50.7	312	4	US-09-851-026-36 Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-10409
; Sequence 10409, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10409
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10409

Query Match 100.0%; Score 75; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTWKIKIAPP 15
DB 185 APSTWKIKIAPP 199

RESULT 2

US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:

MEDIUM TYPE:	Floppy disk
COMPUTER:	Apple Macintosh
OPERATING SYSTEM:	Macintosh
SOFTWARE:	Microsoft Word for Macintosh
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/609,236
FILING DATE:	March 1, 1996
CLASSIFICATION:	514
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	60/002,288
FILING DATE:	August 14, 1995
CLASSIFICATION:	514
ATTORNEY/AGENT INFORMATION:	
NAME:	Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER:	35,423
REFERENCE/DOCKET NUMBER:	D5807
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	713-777-2321
TELEFAX:	713-777-6908
INFORMATION FOR SEQ ID NO:	6:
SEQUENCE CHARACTERISTICS:	
LENGTH:	374
TYPE:	Amino acid
STRANDEDNESS:	
TOPOLOGY:	Linear
MOLECULE TYPE:	Protein
DESCRIPTION:	No
HYPOTHETICAL:	No
ANTI-SENSE:	No
FRAGMENT TYPE:	
ORIGINAL SOURCE:	
STRAIN:	
INDIVIDUAL ISOLATE:	
DEVELOPMENTAL STAGE:	
TISSUE TYPE:	
CELL TYPE:	
CELL LINE:	
US-08-609-236-6	
Query Match	100.0%; Score 75; DB 3; Length 374;
Best Local Similarity	100.0%; Pred. No. 2.9e-05;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 APSTMKIKIAPP 15
Db	320 APSTMKIKIAPP 334
RESULT 3	
US-09-306-446C-2	
Sequence 2, Application US/09306446C	
Patent No. 6372959	
GENERAL INFORMATION:	
APPLICANT:	KIM, Dong Soo
APPLICANT:	KIM, Chul Geun
APPLICANT:	NAM, Yoon Kwon
APPLICANT:	NOH, Jae Koo
APPLICANT:	CHO, Kyou Nam
TITLE OF INVENTION:	EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
FILE REFERENCE:	P06344U0/BAS
CURRENT APPLICATION NUMBER:	US/09/306,446C
CURRENT FILING DATE:	1999-05-06
PRIOR APPLICATION NUMBER:	KR 98/20255
PRIOR FILING DATE:	1998-06-01
NUMBER OF SEQ ID NOS:	33
SOFTWARE:	PatentIn Ver. 2.0
SEQ ID NO 2	
LENGTH:	374
TYPE:	PRT
ORGANISM:	Misgurnus mizolepus
US-09-306-446C-2	


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; SOFTWARE: PERL Program
; SEQ ID NO 731
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match          100.0%; Score 75; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APSTMKIKIAPP 15
      |||||
Db      321 APSTMKIKIAPP 335

RESULT 6
US-08-588-113-2
; Sequence 2, Application US/08588113
; Patent No. 5710003
; GENERAL INFORMATION:
; APPLICANT: McHugh, Kirk M.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5710003ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,113
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: TJU-1652
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-588-113-2

Query Match          100.0%; Score 75; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APSTMKIKIAPP 15
      |||||
Db      322 APSTMKIKIAPP 336

RESULT 7
US-09-949-016-6100
; Sequence 6100, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6100
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6100

Query Match          100.0%; Score 75; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APSTMKIKIAPP 15
      |||||
Db      322 APSTMKIKIAPP 336

RESULT 8
US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-2

Query Match          100.0%; Score 75; DB 3; Length 377;
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Best Local Similarity 100.0%; Pred. No. 2.9e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 APSTMKIKIAPP 15
Db 323 APSTMKIKIAPP 337

RESULT 9
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Farris, Mary
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match 100.0%; Score 75; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
Db 323 APSTMKIKIAPP 337

RESULT 10
US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 100.0%; Score 75; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
Db 323 APSTMKIKIAPP 337

RESULT 11
US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

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Best Local Similarity 100.0%; Pred. No. 3e-05;
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QY 1 APSTMKIKIAPP 15
Db 332 APSTMKIKIAPP 346

RESULT 12
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; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 75; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
Db 345 APSTMKIKIAPP 359

RESULT 13
US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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/ ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ ; FILE REFERENCE: CL001307
/ ; CURRENT APPLICATION NUMBER: US/09/949,016
/ ; CURRENT FILING DATE: 2000-04-14
/ ; PRIOR APPLICATION NUMBER: 60/241,755
/ ; PRIOR FILING DATE: 2000-10-20
/ ; PRIOR APPLICATION NUMBER: 60/237,768
/ ; PRIOR FILING DATE: 2000-10-03
/ ; PRIOR APPLICATION NUMBER: 60/231,498
/ ; PRIOR FILING DATE: 2000-09-08
/ ; NUMBER OF SEQ ID NOS: 207012
/ ; SOFTWARE: FastSeq for Windows Version 4.0
/ ; SEQ ID NO 10757
/ ; LENGTH: 402
/ ; TYPE: PRT
/ ; ORGANISM: Human
/ ; US-09-949-016-10757

Query Match 100.0%; Score 75; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
Db 348 APSTMKIKIAPP 362

RESULT 14
US-09-949-016-11313
/ ; Sequence 11313, Application US/09949016
/ ; Patent No. 6812339
/ ; GENERAL INFORMATION:
/ ; APPLICANT: VENTER, J. Craig et al.
/ ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ ; FILE REFERENCE: CL001307
/ ; CURRENT APPLICATION NUMBER: US/09/949,016
/ ; CURRENT FILING DATE: 2000-04-14
/ ; PRIOR APPLICATION NUMBER: 60/241,755
/ ; PRIOR FILING DATE: 2000-10-20
/ ; PRIOR APPLICATION NUMBER: 60/237,768
/ ; PRIOR FILING DATE: 2000-10-03
/ ; PRIOR APPLICATION NUMBER: 60/231,498
/ ; PRIOR FILING DATE: 2000-09-08
/ ; NUMBER OF SEQ ID NOS: 207012
/ ; SOFTWARE: FastSeq for Windows Version 4.0
/ ; SEQ ID NO 11313
/ ; LENGTH: 404
/ ; TYPE: PRT
/ ; ORGANISM: Human
/ ; US-09-949-016-11313

Query Match 100.0%; Score 75; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
Db 350 APSTMKIKIAPP 364

RESULT 15
US-09-171-337A-7
/ ; Sequence 7, Application US/09171337A
/ ; Patent No. 6300095
/ ; GENERAL INFORMATION:
/ ; APPLICANT: BARREDO FUENTE, Jose Luis
/ ; RODRIGUEZ SAIZ, Marta
/ ; COLLADOS DE LA VIEJA, Alfonso J.
/ ; MORENO VALLE, Migueu Angel
/ ; SALTO MALDONADO, Francisco
/ ; DIEZ GARCIA, Bruno
/ ; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
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/ ; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
/ ; AND -ACTIN AND THEIR USE IN FILAMENTOUS
/ ; FUNGI EXPRESSION, SECRETION AND ANTISENSE
/ ; NUMBER OF SEQUENCES: 20
/ ; CORRESPONDENCE ADDRESS:
/ ; ADDRESSEE: LADAS & PARRY
/ ; STREET: 26 WEST 61 STREET
/ ; CITY: NEW YORK
/ ; STATE: NY
/ ; COUNTRY: USA
/ ; ZIP: 10023
/ ; COMPUTER READABLE FORM:
/ ; MEDIUM TYPE: 3-1/4" Disk 1.44MB
/ ; COMPUTER: IBM PC compatible
/ ; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
/ ; SOFTWARE: WordPerfect 8 for Windows
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/09/171,337A
/ ; FILING DATE: 14-May-1999
/ ; CLASSIFICATION: 536
/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: PCT/ES98/00056
/ ; FILING DATE: 5-MAR-1998
/ ; APPLICATION NUMBER: ES9700482
/ ; FILING DATE: 5-MAR-1997
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: MASS, Clifford J.
/ ; REGISTRATION NUMBER: 30,086
/ ; (C) REF./DOCKET NO.: U-011948-3
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 233288
/ ; INFORMATION FOR SEQ ID NO: 7
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 375 amino acids
/ ; TYPE: amino acids
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: peptide
/ ; ORIGINAL SOURCE:
/ ; ORGANISM: Penicillium chrysogenum
/ ; FEATURE:
/ ; OTHER INFORMATION: amino acid sequence of the -actin
/ ; protein with a molecular weight of
/ ; 41760 Da.
/ ; SEQUENCE DESCRIPTION: SEQ ID NO: 7
/ ; US-09-171-337A-7

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Best Local Similarity 86.7%; Pred. No. 0.00022;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
Db 321 APSTMKIKIAPP 335

Search completed: April 8, 2005, 12:07:40
Job time : 18.5333 secs
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OM protein - protein search, using sw model

Run on: April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds

(without alignments)

116.718 Million cell updates/sec

Title: US-09-423-351C-14

Perfect score: 75

Sequence: 1 APSTMKIKIADPER 15

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Searched: 1418010 seqs, 331997259 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	75	100.0	58	16	US-10-437-963-127939 Sequence 127939
2	75	100.0	72	16	US-10-437-963-153523 Sequence 153523
3	75	100.0	89	15	US-10-424-599-158103 Sequence 158103
4	75	100.0	100	9	US-09-796-692-1768 Sequence 1768, Ap
5	75	100.0	100	9	US-09-796-692-2271 Sequence 2271, Ap
6	75	100.0	100	14	US-10-040-862-1768 Sequence 1768, Ap
7	75	100.0	100	14	US-10-040-862-2271 Sequence 2271, Ap
8	75	100.0	100	15	US-10-057-475B-1768 Sequence 1768, Ap
9	75	100.0	100	15	US-10-057-475B-2271 Sequence 2271, Ap
10	75	100.0	100	15	US-10-154-884B-1768 Sequence 1768, Ap
11	75	100.0	100	15	US-10-154-884B-2271 Sequence 2271, Ap
12	75	100.0	100	16	US-10-764-324-1768 Sequence 1768, Ap
13	75	100.0	100	16	US-10-764-324-2271 Sequence 2271, Ap

14	75	100.0	101	9	US-09-925-300-1732 Sequence 1732, Ap
15	75	100.0	106	15	US-10-424-599-281378 Sequence 281378, Ap
16	75	100.0	110	15	US-10-264-049-4060 Sequence 4060, Ap
17	75	100.0	133	15	US-10-424-599-143033 Sequence 143033, Ap
18	75	100.0	135	15	US-10-424-599-157815 Sequence 157815, Ap
19	75	100.0	145	15	US-10-264-049-4259 Sequence 4259, Ap
20	75	100.0	147	9	US-09-796-692-1239 Sequence 1239, Ap
21	75	100.0	147	9	US-09-796-692-1696 Sequence 1696, Ap
22	75	100.0	147	9	US-09-796-692-2250 Sequence 2250, Ap
23	75	100.0	147	14	US-10-040-862-1239 Sequence 1239, Ap
24	75	100.0	147	14	US-10-040-862-1696 Sequence 1696, Ap
25	75	100.0	147	14	US-10-040-862-2250 Sequence 2250, Ap
26	75	100.0	147	15	US-10-057-475B-1239 Sequence 1239, Ap
27	75	100.0	147	15	US-10-057-475B-1696 Sequence 1696, Ap
28	75	100.0	147	15	US-10-057-475B-2250 Sequence 2250, Ap
29	75	100.0	147	15	US-10-154-884B-1239 Sequence 1239, Ap
30	75	100.0	147	15	US-10-154-884B-1696 Sequence 1696, Ap
31	75	100.0	147	15	US-10-154-884B-2250 Sequence 2250, Ap
32	75	100.0	147	16	US-10-322-281-66 Sequence 66, Appl
33	75	100.0	147	16	US-10-764-324-1239 Sequence 1239, Ap
34	75	100.0	147	16	US-10-764-324-1696 Sequence 1696, Ap
35	75	100.0	147	16	US-10-764-324-2250 Sequence 2250, Ap
36	75	100.0	236	15	US-10-424-599-206389 Sequence 206389, Ap
37	75	100.0	261	15	US-10-424-599-177530 Sequence 177530, Ap
38	75	100.0	342	15	US-10-108-260A-4008 Sequence 4008, Ap
39	75	100.0	371	16	US-10-322-281-68 Sequence 68, Appl
40	75	100.0	375	14	US-10-205-194-93 Sequence 93, Appl
41	75	100.0	375	14	US-10-316-253-88 Sequence 88, Appl
42	75	100.0	375	15	US-10-369-493-5927 Sequence 5927, Ap
43	75	100.0	375	15	US-10-205-331-94 Sequence 94, Appl
44	75	100.0	375	15	US-10-260-708-82 Sequence 82, Appl
45	75	100.0	376	15	US-10-341-434-101 Sequence 101, Appl

ALIGNMENTS

RESULT 1

US-10-437-963-127939
; Sequence 127939, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(93221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 127939
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30340C.1.pap
US-10-437-963-127939

Query Match 100.0%; Score 75; DB 16; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 APSTMKIKIADPER 18

Fri Apr 8 14:14:21 2005

us-09-423-351c-14.rapb

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RESULT 2
US-10-437-963-153523
; Sequence 153523, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 153523
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_53470C.1.pep
US-10-437-963-153523

Query Match          100.0%; Score 75; DB 16; Length 72;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 APSTMKIKIIAPPER 15
Db      18 APSTMKIKIIAPPER 32

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US-10-424-599-158103
; Sequence 158103, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 158103
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(89)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_113787C.1.pep
US-10-424-599-158103

Query Match          100.0%; Score 75; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
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Db      35 APSTMKIKIIAPPER 49

RESULT 4
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US-09-796-692-1768
; Sequence 1768, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1768

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Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 APSTMKIKIIAPPER 15
Db      66 APSTMKIKIIAPPER 80

RESULT 5
US-09-796-692-2271
; Sequence 2271, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
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; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-2271

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Query Match 100.0%; Score 75; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 APSTMKIKIAPP 15
Db 66 APSTMKIKIAPP 80

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; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-28
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; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07

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; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1768

```

```

Query Match 100.0%; Score 75; DB 14; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 APSTMKIKIAPP 15
Db 66 APSTMKIKIAPP 80

```

```

RESULT 7
US-10-040-862-2271
; Sequence 2271, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-2271

```

```

Query Match 100.0%; Score 75; DB 14; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 APSTMKIKIAPP 15

```

Db

66 APSTWKIKIAPP 80

|||||

US-10-057-475B-1768

Sequence 1768, Application US/10057475B

Publication No. US20040002068A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Clapper, Jonathan David

APPLICANT: Wang, Aijun

APPLICANT: Ordonez, Nadia

APPLICANT: Carter, Lauren

APPLICANT: McNeill, Patricia Dianne

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-014402US

CURRENT APPLICATION NUMBER: US/10/057,475B

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: US 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: US 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 60/222,903

PRIOR FILING DATE: 2000-08-03

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 10979

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1768

LENGTH: 100

TYPE: PRT

ORGANISM: Homo sapiens

US-10-057-475B-2271

Query Match 100.0%; Score 75; DB 15; Length 100;

Best Local Similarity 100.0%; Pred. No. 7.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTWKIKIAPP 15

|||||

Db 66 APSTWKIKIAPP 80

|||||

US-10-057-475B-1768

Sequence 1768, Application US/10057475B

Publication No. US20040002068A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Clapper, Jonathan David

APPLICANT: Wang, Aijun

APPLICANT: Ordonez, Nadia

APPLICANT: Carter, Lauren

APPLICANT: McNeill, Patricia Dianne

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-014402US

CURRENT APPLICATION NUMBER: US/10/057,475B

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: US 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: US 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 60/222,903

PRIOR FILING DATE: 2000-08-03

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 10979

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1768

LENGTH: 100

TYPE: PRT

ORGANISM: Homo sapiens

US-10-057-475B-1768

Query Match 100.0%; Score 75; DB 15; Length 100;

Best Local Similarity 100.0%; Pred. No. 7.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTWKIKIAPP 15

|||||

Db 66 APSTWKIKIAPP 80

|||||

US-10-057-475B-2271

Sequence 2271, Application US/10057475B

Publication No. US20040002068A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Clapper, Jonathan David

APPLICANT: Wang, Aijun

APPLICANT: Ordonez, Nadia

APPLICANT: Carter, Lauren

APPLICANT: McNeill, Patricia Dianne

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-013521US

CURRENT APPLICATION NUMBER: US/10/154,884B

CURRENT FILING DATE: 2002-05-23

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/202,084

Result 10

US-10-154-884B-1768

Sequence 1768, Application US/10154884B

Publication No. US20040005561A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Retter, Marc W.

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-013521US

CURRENT APPLICATION NUMBER: US/10/154,884B

CURRENT FILING DATE: 2002-05-23

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/202,084

;
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-1768

Query Match 100.0%; Score 75; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
|||||
Db 66 APSTMKIKIAPP 80

RESULT 11
US-10-154-884B-2271
; Sequence 2271, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-2271

Query Match 100.0%; Score 75; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
|||||
Db 66 APSTMKIKIAPP 80

RESULT 12
US-10-764-324-1768
; Sequence 1768, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-1768

Query Match 100.0%; Score 75; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APSTMKIKIAPP 15
|||||
Db 66 APSTMKIKIAPP 80

RESULT 13
US-10-764-324-2271
; Sequence 2271, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23

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; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-2271

Query Match      100.0%; Score 75; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.8e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY      1 APSTMKIKIIPPER 15
Db      66 APSTMKIKIIPPER 80

RESULT 14
US-09-925-300-1732
; Sequence 1732, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1732
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (68)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (78)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

```

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; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (91)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1732

Query Match      100.0%; Score 75; DB 9; Length 101;
Best Local Similarity 100.0%; Pred. No. 7.9e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY      1 APSTMKIKIIPPER 15
Db      35 APSTMKIKIIPPER 49

RESULT 15
US-10-424-599-281378
; Sequence 281378, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 281378
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_96105C.1.pcp
US-10-424-599-281378

Query Match      100.0%; Score 75; DB 15; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.3e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY      1 APSTMKIKIIPPER 15
Db      52 APSTMKIKIIPPER 66

Search completed: April 8, 2005, 12:51:02
Job time : 43.6667 secs

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; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1239
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1239

Query Match 100.0%; Score 73; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASSSSLEKSYELPDG 15
| | | | | | | | | | | | | | | | | | | | |
Db 3 ASSSSLEKSYELPDG 17

RESULT 2

US-09-796-692-1696
; Sequence 1696, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1696
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1696

Query Match 100.0%; Score 73; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASSSSLEKSYELPDG 15
| | | | | | | | | | | | | | | | | | | | |
Db 3 ASSSSLEKSYELPDG 17

RESULT 3

US-09-796-692-2250
; Sequence 2250, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2250
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-2250

Query Match 100.0%; Score 73; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASSSSLEKSYELPDG 15
| | | | | | | | | | | | | | | | | | | | |
Db 3 ASSSSLEKSYELPDG 17

RESULT 4
US-10-040-862-1239
; Sequence 1239, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545

```

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1239
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1239

```

```

Query Match 100.0%; Score 73; DB 14; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ASSSLEKSYELPDG 15
Db 3 ASSSLEKSYELPDG 17

```

```

RESULT 5
US-10-040-862-1696
; Sequence 1696, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1239
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1239

```

```

; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1696
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1696

```

```

Query Match 100.0%; Score 73; DB 14; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ASSSLEKSYELPDG 15
Db 3 ASSSLEKSYELPDG 17

```

```

RESULT 6
US-10-040-862-2250
; Sequence 2250, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2250
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-2250

```

```

Query Match 100.0%; Score 73; DB 14; Length 147;

```

```

APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1696
LENGTH: 147
TYPE: PRT
ORGANISM: Homo sapiens
US-10-057-475B-1696

Query Match 100.0%; Score 73; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
Db 3 ASSSSLEKSYELPDG 17
|||||
|||||

RESULT 9
US-10-057-475B-2250
Sequence 2250, Application US/10057475B
Publication No. US20040002068A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545

```

```

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2250
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-2250

```

```

Query Match      100.0%; Score 73; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 ASSSSLEKSYELPDG 15
        |||||
DB      3 ASSSSLEKSYELPDG 17

```

```

RESULT 10
US-10-154-884B-1239
; Sequence 1239, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1239
; LENGTH: 147

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-1239

```

```

Query Match      100.0%; Score 73; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 ASSSSLEKSYELPDG 15
        |||||
DB      3 ASSSSLEKSYELPDG 17

```

```

RESULT 11
US-10-154-884B-1696
; Sequence 1696, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1696
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-1696

```

```

Query Match      100.0%; Score 73; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 ASSSSLEKSYELPDG 15
        |||||
DB      3 ASSSSLEKSYELPDG 17

```

```

RESULT 12
US-10-154-884B-2250
; Sequence 2250, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.

```

```

; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2250
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-2250

Query Match      100.0%; Score 73; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
Db 3 ASSSSLEKSYELPDG 17

RESULT 13
US-10-322-281-66
; Sequence 66, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-66

Query Match      100.0%; Score 73; DB 16; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
Db 5 ASSSSLEKSYELPDG 19
```

```

RESULT 14
US-10-764-324-1239
; Sequence 1239, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1239
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-1239

Query Match      100.0%; Score 73; DB 16; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
Db 3 ASSSSLEKSYELPDG 17

RESULT 15
US-10-764-324-1696
; Sequence 1696, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
```



```

; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1696
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-1696

Query Match      100.0%; Score 73; DB 16; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ASSSSLEKSYELPDG 15
      |||||
Db      3  ASSSSLEKSYELPDG 17

```

Search completed: April 8, 2005, 12:51:01
Job time : 42.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.3333 Seconds
(without alignment)
154.634 Million cell updates/sec

Title: US-09-423-351c-12

Perfect score: 75

Sequence: 1 RGYSFTTTAEREIVR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	195	2 S20097	actin 85c - potato
2	75	100.0	325	2 JC2008	actin homolog prot
3	75	100.0	328	2 S05430	actin beta - grass
4	75	100.0	331	2 S24409	actin - brown alga
5	75	100.0	336	2 T04085	actin - maize (fra
6	75	100.0	362	2 A26559	actin type 5, cyto
7	75	100.0	365	2 S49007	actin - Pythium ir
8	75	100.0	365	2 A37431	actin, type 1 - Em
9	75	100.0	370	2 A29664	actin - sea urchin
10	75	100.0	374	1 ATBOB	actin beta - bovin
11	75	100.0	374	1 ATBOG	actin gamma - bovi
12	75	100.0	374	2 S5818	gamma-actin - huma
13	75	100.0	375	1 ATRTC	actin beta - rat
14	75	100.0	375	1 A48324	actin beta, cytosk
15	75	100.0	375	1 ATAX	actin - Acanthamo
16	75	100.0	375	1 ATCHB	actin beta - chick
17	75	100.0	375	1 ATDO	actin - slime mold
18	75	100.0	375	1 ATDUB	actin beta - human
19	75	100.0	375	1 ATHUG	actin gamma 1 - hu
20	75	100.0	375	1 ATWSB	actin beta - mouse
21	75	100.0	375	1 ATMSG	actin gamma - mous
22	75	100.0	375	1 ATRRB	actin beta, non-mu
23	75	100.0	375	1 S11222	actin gamma, cytos
24	75	100.0	375	1 ATUN	actin - Phytophtho
25	75	100.0	375	2 S33386	actin, cytosolic (
26	75	100.0	375	2 JE0415	actin B - Phytopht
27	75	100.0	375	2 S71125	actin beta-2, cyto
28	75	100.0	375	2 S71124	actin beta-1, cyto
29	75	100.0	375	2 S71126	actin beta, cyto

30 75 100.0 375 2 A55001 actin beta - goose
31 75 100.0 375 2 S03126 actin - imperfect
32 75 100.0 376 1 ATFF7 actin 7 - fruit fl
33 75 100.0 376 1 A43552 actin gamma, cytos
34 75 100.0 376 1 ATFY actin - slime mold
35 75 100.0 376 1 ATRZ7 actin 7 - rice
36 75 100.0 376 1 ATURS actin Cy1 - sea ur
37 75 100.0 376 2 B23412 actin 12 - slime m
38 75 100.0 376 2 A48449 Actin-1A - nematod
39 75 100.0 376 2 S04538 actin 87E - fruit
40 75 100.0 376 2 JC1246 actin - fruit fly
41 75 100.0 376 2 A45634 actin - Cryptospor
42 75 100.0 376 2 JS0189 actin, cytosolic -
43 75 100.0 376 2 JS0190 actin, muscle - st
44 75 100.0 376 2 S07288 actin 15A - sea ur
45 75 100.0 376 2 S09578 actin - sea urchin

ALIGNMENTS

RESULT 1

S20097

actin 85c - potato (fragment)

C:Species: Solanum tuberosum (potato)

C>Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004

C:Accession: S20097

R:Drouin, G.; Dover, G.A.

J. Mol. Evol. 31, 132-150, 1990

A>Title: Independent gene evolution in the potato actin gene family demonstrated by phy

A:Reference number: S20092; MUID:91012599; PMID:2120451

A:Accession: S20097

A:Molecule type: DNA

A:Residues: 1-195 <DRO>

A:Cross-references: UNIPROT:P30170; EMBL:X55747; NID:G21541; PIDN:CAA39277.1; PID:G13453

C:Genetics:

A:introns: 132/1

C:Superfamily: actin

C:Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 75; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAEREIVR 15

Db 178 RGYSFTTTAEREIVR 192

RESULT 2

JC2008

actin homolog protein - red swamp crayfish

C:Species: Procambarus clarkii (red swamp crayfish)

C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000

C:Accession: JC2008

R:Kang, W.K.; Naya, Y.

Gene 133, 303-304, 1993

A>Title: Sequence of the cDNA encoding an actin homolog in the crayfish Procambarus cla

A:Reference number: JC2008; MUID:94040829; PMID:8224920

A:Accession: JC2008

A:Molecule type: mRNA

A:Residues: 1-325 <KAN>

A:Cross-references: GB:D14612; NID:G434784; PIDN:BA03463.1; PID:G434785

A:Experimental source: muscle

C:Superfamily: actin

C:Keywords: muscle contraction

Query Match 100.0%; Score 75; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAEREIVR 15

Db 178 RGYSFTTTAEREIVR 192

Fri Apr 8 14:14:19 2005

us-09-423-351c-12.rpr

Db 146 RGYSTTTTAREIVR 160

RESULT 3

S05430

actin beta - grass carp

C:Species: Ctenopharyngodon idella (grass carp)

C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C:Accession: S05430

R:Li, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.

Nucleic Acids Res. 17, 5850, 1989

A:Title: The beta-actin gene of carp (Ctenopharyngodon idella).

A:Reference number: S05430; MUID:89345185; PMID:2762162

A:Accession: S05430

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-328 <LIU>

A:Cross-references: UNIPROT:P83751; EMBL:M25013

C:Genetics:

A:Introns: 41/3; 121/3; 268/1

C:Superfamily: actin

C:Keywords: cytoskeleton; methylated amino acid

F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 328;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAREIVR 15

|||||

Db 196 RGYSTTTTAREIVR 210

RESULT 4

S24409

actin - brown alga (Costaria costata) (fragment)

C:Species: Costaria costata

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C:Accession: S24409

R:Bhattacharya, D.; Stickel, S.K.; Sogin, M.L.

J. Mol. Evol. 33, 525-536, 1991

A:Title: Molecular phylogenetic analysis of actin genic regions from Achlya bisexualis

A:Reference number: S24408; MUID:92139446; PMID:1779434

A:Accession: S24409

A:Molecule type: mRNA

A:Residues: 1-331 <BHA>

A:Cross-references: UNIPROT:P30161; EMBL:X59937; NID:gl7956; PIDN:CAA42560.1; PID:gl7957

C:Superfamily: actin

C:Keywords: methylated amino acid

F;29/Modified site: 3'-methylhistidine (His) #status predicted

Query Match

Best Local Similarity 100.0%; Score 75; DB 2; Length 331;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAREIVR 15

|||||

Db 152 RGYSTTTTAREIVR 166

RESULT 5

T04085

actin - maize (fragment)

C:Species: Zea mays (maize)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T04085

R:de Sa, M.; Drouin, G.

Mol. Biol. Evol. 13, 1198-1212, 1996

A:Title: Phylogeny and substitution rates of angiosperm actin genes.

A:Reference number: Z15197; MUID:97051711; PMID:8896372

A:Accession: T04085

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-336 <DES>

A:Cross-references: UNIPROT:P93638; EMBL:U60513; NID:gl498392; PIDN:AAB40107.1; PID:gl49

C:Genetics:

A:Gene: Maz63

A>Note: Intron positions not resolved (incomplete sequence)

C:Superfamily: actin

C:Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 75; DB 2; Length 336;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAREIVR 15

|||||

Db 178 RGYSTTTTAREIVR 192

RESULT 6

A26559

actin type 5, cytosolic - chicken

C:Species: Gallus gallus (chicken)

C>Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997

C:Accession: A26559

R:Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.

Mol. Cell. Biol. 5, 1151-1162, 1985

A:Reference number: A26559; MUID:85213487; PMID:4000121

A:Accession: A26559

A:Molecule type: DNA

A:Residues: 1-362 <BER>

C:Superfamily: actin

C:Keywords: cytosol; methylated amino acid

F;74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match

Best Local Similarity 100.0%; Score 75; DB 2; Length 362;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAREIVR 15

|||||

Db 197 RGYSTTTTAREIVR 211

RESULT 7

S49007

actin - Pythium irregulare (fragment)

C:Species: Pythium irregulare

C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999

C:Accession: S49007

R:Bhattacharya, D.; Stickel, S.K.

J. Mol. Evol. 39, 56-61, 1994

A:Title: Sequence analysis of duplicated actin genes in Lagenidium giganteum and Pythium

A:Reference number: S49007; MUID:94343543; PMID:8084873

A:Accession: S49007

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-365 <BHA>

A:Cross-references: EMBL:X76725

A:Experimental source: strain P3804

C:Superfamily: actin

Query Match

Best Local Similarity 100.0%; Score 75; DB 2; Length 365;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAREIVR 15

|||||

Db 186 RGYSTTTTAREIVR 200

RESULT 8

A37431

actin, type 1 - Emiliana huxleyi (fragment)

C:Species: Emiliana huxleyi

C>Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
A:Accession: A37431
R:Bhattacharya, D.; Stickle, S.K.; Sogin, M.L.
Mol. Biol. Evol. 10, 689-703, 1993
A>Title: Isolation and molecular phylogenetic analysis of actin-coding regions from Emil
A:Reference number: A37431; MUID:93330051; PMID:7687735
A:Contents: CCM2379
A:Accession: A37431
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-365 <SHA>
A:Cross-references: UNIPROT:Q41205; GB:S64188; NID:G404406; PIDN:AAB27626.1; PID:G404407
A>Note: sequence extracted from NCBI backbone (NCBIN:135711, NCBIP:135712)
C:Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAEREIVR 15
|||||
DB 186 RGYSTTTTAEREIVR 200
|||||

RESULT 9
A29664
actin - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
A:Accession: A29664
R:Crain Jr., W.R.; Boshar, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D.
J. Mol. Evol. 25, 37-45, 1987
A>Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with
A:Reference number: A29664; MUID:87311761; PMID:3114500
A:Accession: A29664
A:Molecule type: DNA
A:Residues: 1-370 <CRA>
A:Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
A>Note: the authors translated the codon CAG for residue 260 as Glu
C:Superfamily: actin
C:Keywords: methylated amino acid
F:7/3/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAEREIVR 15
|||||
DB 193 RGYSTTTTAEREIVR 207
|||||

RESULT 10
ATBOG
actin beta - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
A:Accession: A14185; A39105; A02999; A14185
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A>Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P60712
A>Note: only peptides that differed in composition from the corresponding peptides of ra
R:Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A>Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analy
A:Reference number: A39105; MUID:84032385; PMID:6195151
A:Accession: A39105
A:Molecule type: mRNA

A:Residues: 76-227;344-374 <DEG>
A:Cross-references: GB:K00622; GB:K00623
A>Note: actins beta and gamma were not distinguished in this study
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F:7/2/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAEREIVR 15
|||||
DB 195 RGYSTTTTAEREIVR 209
|||||

RESULT 11
ATBOG
actin gamma - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
A:Accession: B14185; A02999
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A>Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: B14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P02571
A>Note: only peptides that differed in composition from the corresponding peptides of ra
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
F:7/2/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAEREIVR 15
|||||
DB 195 RGYSTTTTAEREIVR 209
|||||

RESULT 12
JC5818
gamma-actin - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
A:Accession: JC5818; PC4501
R:Haushildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens
Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A>Title: Actin: A target of lipopolysaccharide-induced phosphorylation in human monocytes
A:Reference number: JC5818; MUID:98096379; PMID:9434766
A:Accession: JC5818
A:Molecule type: protein
A:Residues: 1-374 <HAU>
A:Cross-references: UNIPROT:P02571
A:Experimental source: monocyte
A:Accession: PC4501
A:Molecule type: protein
A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A:Experimental source: monocyte
C:Comment: This protein is involved in a signal transduction that eventually leads to m
C:Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

ATAX
actin - Acanthamoeba castellanii
C;Species: Acanthamoeba castellanii
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A92886; A03004
R;Nellen, W.; Gallwitz, D.
J. Mol. Biol. 159, 1-18, 1982
A;Title: Actin genes and actin messenger RNA in Acanthamoeba castellanii. Nucleotide seq
A;Reference number: A92886; MUID:83033627; PMID:6290670
A;Accession: A92886
A;Molecule type: DNA
A;Residues: 1-375 <N>
A;Cross-references: UNIPROT:P02578; GB:V00002; GB:J01016; NID:95565; PIDN:CAA23399.1; PI
C;Comment: There are at least three actin genes in A. castellanii.
C;Genetics:
A;Introns: 105/3
C;Superfamily: actin
C;Keywords: methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSTTTAEREIVR 15
Db 196 RGYSTTTAEREIVR 210

Search completed: April 8, 2005, 10:53:07
Job time : 9.3333 secs

RESULT 13
actin beta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
C;Accession: A38571; A02999
R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A;Reference number: A38571; MUID:83168920; PMID:6300777
A;Accession: A38571
A;Molecule type: DNA
A;Residues: 1-375 <NUD>
A;Cross-references: GB:J00691; NID:9202653; PIDN:AAA0657.1; PID:9202654
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C;Genetics:
A;Introns: 41/3; 121/3; 268/1; 328/3
C;Superfamily: actin
C;Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;
F;2-375/Product: actin beta #status predicted <MAT>
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSTTTAEREIVR 15
Db 196 RGYSTTTAEREIVR 210

RESULT 14
actin beta, cytoskeletal - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: A48324
R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
DNA Seq. 1, 125-136, 1990
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A;Reference number: A48324; MUID:92190540; PMID:2134183
A;Accession: A48324
A;Molecule type: DNA
A;Residues: 1-375 <LIU>
A;Cross-references: UNIPROT:P83750; GB:M24113; NID:9213041; PIDN:AA6886.1; PID:9213042
A;Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 a
7 as Pro
A;Note: the authors failed to translated the codon GGT for residue 42 as Gly
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C;Genetics:
A;Introns: 41/3; 121/3; 268/3; 328/3
C;Superfamily: actin
C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F;2-375/Product: actin beta, cytoskeletal #status predicted <MAT>
F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSTTTAEREIVR 15
Db 196 RGYSTTTAEREIVR 210

RESULT 15

```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-12
Perfect score: 75
Sequence: 1 RGYSTTTAEREIVR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03 : *
1: uniprot_sprot : *
2: uniprot_trembl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	33	2 Q6V107	Q6V107 mus spretus
2	75	100.0	39	2 Q6S3E7	Q6S3E7 poecilia re
3	75	100.0	56	2 Q91L43	Q91L43 trebouxia j
4	75	100.0	93	2 Q6VQP9	Q6VQP9 romalea mic
5	75	100.0	101	2 Q61569	Q61569 osteragla
6	75	100.0	104	2 Q11210	Q11210 macaca fasc
7	75	100.0	109	2 Q28916	Q28916 macaca fusc
8	75	100.0	124	2 Q9FY43	Q9FY43 trebouxia j
9	75	100.0	125	2 Q802E1	Q802E1 zoarces viv
10	75	100.0	125	2 Q802E2	Q802E2 pachycara b
11	75	100.0	128	2 Q852Q7	Q852Q7 marchantia
12	75	100.0	130	2 Q865G0	Q865G0 capra hircu
13	75	100.0	132	2 Q91A84	Q91A84 stizostedio
14	75	100.0	133	2 Q9U4L7	Q9U4L7 agenisaspis
15	75	100.0	133	2 Q9U4L8	Q9U4L8 agenisaspis
16	75	100.0	133	2 Q9U4L9	Q9U4L9 agenisaspis
17	75	100.0	133	2 Q9U4M0	Q9U4M0 agenisaspis
18	75	100.0	136	2 Q9S5V6	Q9S5V6 ixodes scap
19	75	100.0	136	2 Q89054	Q89054 mus musculu
20	75	100.0	137	2 Q8H1A1	Q8H1A1 nicotiana b
21	75	100.0	142	2 Q9SGH4	Q9SGH4 oryctolagus
22	75	100.0	145	2 Q91L42	Q91L42 trebouxia j
23	75	100.0	146	2 Q9Y191	Q9Y191 plecoglossu
24	75	100.0	150	2 Q68AX1	Q68AX1 cynops pyr
25	75	100.0	159	2 Q8MVL3	Q8MVL3 boltenia vi
26	75	100.0	160	2 Q8T6A7	Q8T6A7 trichinella
27	75	100.0	160	2 Q9NAS3	Q9NAS3 blattella g
28	75	100.0	167	2 Q76D36	Q76D36 costus spec
29	75	100.0	167	2 Q76D37	Q76D37 costus spec
30	75	100.0	169	2 Q8SPK6	Q8SPK6 sus scrofa
31	75	100.0	171	2 Q766D6	Q766D6 phyllostach

32	75	100.0	171	2 Q7XAK3	Q7XAK3 asparagus o
33	75	100.0	171	2 Q8JH59	Q8JH59 chelydra se
34	75	100.0	171	2 Q6GXE6	Q6GXE6 lepisosteus
35	75	100.0	171	2 Q7ZWS9	Q7ZWS9 rana catesb
36	75	100.0	172	2 Q869B3	Q869B3 botryllus s
37	75	100.0	173	2 Q6RX10	Q6RX10 ficus caric
38	75	100.0	174	2 Q819W1	Q819W1 biomphalari
39	75	100.0	174	2 Q819W2	Q819W2 biomphalari
40	75	100.0	174	2 Q819W3	Q819W3 biomphalari
41	75	100.0	174	2 Q819W4	Q819W4 biomphalari
42	75	100.0	174	2 Q819W5	Q819W5 biomphalari
43	75	100.0	174	2 Q819W6	Q819W6 helisoma an
44	75	100.0	174	2 Q819W7	Q819W7 helisoma tr
45	75	100.0	174	2 Q819W8	Q819W8 biomphalari

ALIGNMENTS

RESULT 1
Q6V107 PRELIMINARY; PRT; 33 AA.
AC Q6V107;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Beta-actin (Fragment).
GN Name=Actb;
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cabrera-Luque J.M., Prieto-Alamo M.J., Pueyo C.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY355144; AAQ55830.1; -.
FT NON_TER 1
FT NON_TER 33
SQ SEQUENCE 33 AA; 3892 MW; 48ACD0E5344AA20B CRC64;

Query Match 100.0%; Score 75; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGYSTTTAEREIVR 15
Db 8 RGYSTTTAEREIVR 22

RESULT 2
Q6S3E7 PRELIMINARY; PRT; 39 AA.
ID Q6S3E7;
AC Q6S3E7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Beta-actin (Fragment).
OS Poecilia reticulata (Guppy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Poecilia.
OX NCBI_TaxID=8081;
RN [1]
RP SEQUENCE FROM N.A.
RA Hallgren S.L.E., Olsen H.K.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY478389; AAR99700.1; -.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4546 MW; 7BED3DB5437E4D49 CRC64;

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Query Match      100.0%; Score 75; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEIVR 15
Db 20 RGYSTTTTAAEIVR 34

RESULT 3
Q9LL43
ID Q9LL43 PRELIMINARY; PRT; 56 AA.
AC Q9LL43
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Actin type I (Fragment).
OS Trebouxia jamesii.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxioophyceae;
OC Microthamniales; Trebouxia.
OX NCBI_TaxID=53267;
RN [1]
RP SEQUENCE FROM N.A.
RA Kroken S., Taylor J.W.;
RT "Phylogenetic species, reproductive mode, and specificity of the green
RT alga Trebouxia forming lichens with the fungal genus Letharia.";
RL Bryologist 103:645-660(2000).
DR EMBL; AF242472; AAF78028.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 56
FT NON_TER 56
SQ SEQUENCE 56 AA; 6357 MW; 64F701537B21BD32 CRC64;

Query Match      100.0%; Score 75; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEIVR 15
Db 6 RGYSTTTTAAEIVR 20

RESULT 4
Q6VQP9
ID Q6VQP9 PRELIMINARY; PRT; 93 AA.
AC Q6VQP9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Actin (Fragment).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE FROM N.A.
RA Fei H., Martin T., Jaskowiak K., Hatle J., Borst D.W.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY331667; AAQ24502.1; -.
FT NON_TER 1
FT NON_TER 93
SQ SEQUENCE 93 AA; 10698 MW; 5635F5335A532256 CRC64;

Query Match      100.0%; Score 75; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEIVR 15
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Db 38 RGYSTTTTAAEIVR 52

RESULT 5
O61569
ID O61569 PRELIMINARY; PRT; 101 AA.
AC O61569;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Ostertagia ostertagi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
OX NCBI_TaxID=6317;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20233682; PubMed=10769181; DOI=10.1042/0264-6021:3470763;
RA Moore J., Tetley L., Devaney E.;
RT "Identification of abundant mRNAs from the third stage larvae of the
RT parasitic nematode, Ostertagia ostertagi.";
RL Biochem. J. 347:763-770(2000).
DR EMBL; AF052043; AAC06292.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 101
FT NON_TER 101
SQ SEQUENCE 101 AA; 11499 MW; 7AF3A21892AD0D75 CRC64;

Query Match      100.0%; Score 75; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAAEIVR 15
Db 33 RGYSTTTTAAEIVR 47

RESULT 6
Q11210
ID Q11210 PRELIMINARY; PRT; 104 AA.
AC Q11210;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Hino A., Tokuyama Y., Kobayashi M., Yano M., Weir B., Takeda J.,
RA Bell G.I., Macdonald R.L.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20576; AAA62435.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 104
FT NON_TER 104
SQ SEQUENCE 104 AA; 11438 MW; 3610F3FEFA370C91 CRC64;

Query Match      100.0%; Score 75; DB 2; Length 104;
```


Best Local Similarity 100.0%; Pred. No. 1.4e-05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
DB 67 RGYSTTTAEREIVR 81

RESULT 7

ID Q28916 PRELIMINARY; PRT; 109 AA.
AC Q28916;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Actin (Fragment)
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071113; PubMed=7577717; DOI=10.1016/0960-0760(95)00157-U;
RA Yamada-Mouri N., Hirata S., Hayashi M., Kato J.;
RT "Analysis of the expression and the first exon of aromatase mRNA in monkey brain";
RL J. Steroid Biochem. Mol. Biol. 55:17-23(1995).
DR EMBL; S79782; AAB35618.2; -;
DR HSSP; P10983; 1DAX.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12333 MW; 64A64E108CDDA54C CRC64;

Query Match 100.0%; Score 75; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
DB 81 RGYSTTTAEREIVR 95

RESULT 8

ID Q9FY43 PRELIMINARY; PRT; 124 AA.
AC Q9FY43;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Actin type I (Fragment).
OS Trebouxia jamesii 'vulpinae'.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae;
OC Microthamniales; Trebouxia.
OX NCBI_TaxID=134429;
RN [1]
RP SEQUENCE FROM N.A.
RA Kroken S., Taylor J.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY005404; AAF97494.1; -;
DR HSSP; P02577; 1NWI.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.

DR PRINTS; PR00190; ACTIN.
KW Structural protein.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13781 MW; 83AF18D241C8CD8E CRC64;

Query Match 100.0%; Score 75; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.7e-05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
DB 74 RGYSTTTAEREIVR 88

RESULT 9

ID Q802E1 PRELIMINARY; PRT; 125 AA.
AC Q802E1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta actin (Fragment).
GN Name=ACT-B;
OS Zoarces viviparus (Belpout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Zoarcoidei;
OC Zoarcidae; Zoarces.
OX NCBI_TaxID=48416;
RN [1]
RP SEQUENCE FROM N.A.
RA Lucassen M., Sokolov E., Poertner H.-O.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.

DR EMBL; AV227658; AA072722.1; -;
DR HSSP; P60712; 1HLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.

DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 125

SQ SEQUENCE 125 AA; 14100 MW; 7B33EA4CF5EA88B0 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
DB 110 RGYSTTTAEREIVR 124

RESULT 10

ID Q802E2 PRELIMINARY; PRT; 125 AA.
AC Q802E2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta actin (Fragment).
GN Name=ACT-B;
OS Pachycara brachycephalum (Antarctic eelpout) (Austrolycichthys brachycephalum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Zoarcidae;
 OC Zoarcidae; Pachycara.
 OX NCBI_TaxID=36221;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lucassen M., Sokolov E., Poertner H.-O.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.
 CC EMBL; AY227657; AAO2721.1; -.
 DR HSP; P60712; 1HLU.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
 KW Structural protein.
 FT NON_TER 1
 FT NON_TER 125
 FT SEQUENCE 125 AA; 14100 MW; 7B33EA4CF5EA88B0 CRC64;
 SQ
 Query Match 100.0%; Score 75; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGYSFTTTAREIVR 15
 DB 110 RGYSFTTTAREIVR 124
 RESULT 11
 Q85207 PRELIMINARY; PRT; 128 AA.
 ID Q85207
 AC Q85207;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Actin (Fragment).
 GN Name=MpAct1;
 OS Marchantia polymorpha (Liverwort).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
 OC Marchantiopsida; Marchantiales; Marchantiaceae;
 OC Marchantiaceae; Marchantia.
 OX NCBI_TaxID=3197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ahida Y., Fujii Y., Hirata T.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB100427; BAC55601.1; -.
 DR HSP; P02577; 1NM1.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 FT NON_TER 128
 FT SEQUENCE 128 AA; 14527 MW; 53A33892EB2E608C CRC64;
 SQ
 Query Match 100.0%; Score 75; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGYSFTTTAREIVR 15
 DB 32 RGYSFTTTAREIVR 46
 RESULT 12
 Q865G0 PRELIMINARY; PRT; 130 AA.
 ID Q865G0

Q865G0;
 01-JUN-2003 (TrEMBLrel. 24, Created)
 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-actin (Fragment).
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sharnila C., Reddy P.G.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.
 CC EMBL; AF481159; AAO49278.1; -.
 DR HSP; P60712; 1HLU.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
 KW Structural protein.
 FT NON_TER 1
 FT NON_TER 130
 FT SEQUENCE 130 AA; 14728 MW; E817FD365B33EA3F CRC64;
 SQ
 Query Match 100.0%; Score 75; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGYSFTTTAREIVR 15
 DB 111 RGYSFTTTAREIVR 125
 RESULT 13
 Q91A84 PRELIMINARY; PRT; 132 AA.
 ID Q91A84
 AC Q91A84;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta actin (Fragment).
 OS Stizostedion vitreum.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
 OC Percidae; Stizostedion.
 OX NCBI_TaxID=57868;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Dermal sarcoma;
 RC MEDLINE=21109119; PubMed=11162816; DOI=10.1006/viro.2000.0731;
 RA Rovnak J., Casey J.W., Quackenbush S.L.;
 RT "Intracellular targeting of walleye dermal sarcoma virus Orf A (rv-
 cyclin).";
 RL Virology 280:31-40(2001).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.
 CC EMBL; AF219944; AAF31439.1; -.
 DR HSP; P60712; 1HLU.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.

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DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 1486 MW; D78E91FB00A65E8E CRC64;

Query Match
Best Local Similarity 100.0%; Score 75; DB 2; Length 132;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAREIVR 15
DB 107 RGYSTTTTAREIVR 121

RESULT 14
Q9U4L7 PRELIMINARY; PRT; 133 AA.
AC Q9U4L7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 2 (Fragment)
OS Ageniapis citricola.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
OC Encyrtidae; Encyrtinae; Ageniapis.
OX NCBI_TaxID=105762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Taiwan population;
RA Hoy M.A., Jeyaprasath A., Morakote R., Lo P.K.C., Nguyen R.;
RT "Genomic analyses of two populations of Ageniapis citricola
(Hymenoptera: Encyrtidae) suggest that a cryptic species may exist.";
RL Biol. Control 17:1-10(2000).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF164630; AAF22278.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR PRINTS; PRO0190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 14955 MW; 27DFC1FF30D4984F CRC64;

Query Match
Best Local Similarity 100.0%; Score 75; DB 2; Length 133;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAREIVR 15
DB 108 RGYSTTTTAREIVR 122

RESULT 15
Q9U4L8 PRELIMINARY; PRT; 133 AA.
AC Q9U4L8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 1 (Fragment)
OS Ageniapis citricola.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
OC Encyrtidae; Encyrtinae; Ageniapis.
```

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OX NCBI_TaxID=105762;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Taiwan population;
RA Hoy M.A., Jeyaprasath A., Morakote R., Lo P.K.C., Nguyen R.;
RT "Genomic analyses of two populations of Ageniapis citricola
(Hymenoptera: Encyrtidae) suggest that a cryptic species may exist.";
RL Biol. Control 17:1-10(2000).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF164630; AAF22278.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR PRINTS; PRO0190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 14941 MW; 62CB94EF37A39F3F CRC64;

Query Match
Best Local Similarity 100.0%; Score 75; DB 2; Length 133;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAREIVR 15
DB 108 RGYSTTTTAREIVR 122

Search completed: April 8, 2005, 12:03:13
Job time : 57.8667 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-13

Perfect score: 73

Sequence: 1 ASSSSLEKSYELPDG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	15	2 AAW92539	Beta-acti
2	73	100.0	147	4 AAM80875	Aam80875 Human hae
3	73	100.0	147	4 AAM81886	Aam81886 Human hae
4	73	100.0	147	4 AAM81332	Aam81332 Human hae
5	73	100.0	149	8 ABO84771	ABO84771 Human can
6	73	100.0	153	4 AEG15497	Abg15497 Novel hum
7	73	100.0	157	5 ABP42724	Abp42724 Human ova
8	73	100.0	168	5 ABP42912	Abp42912 Human ova
9	73	100.0	185	6 ABU70840	Abu70840 Human adi
10	73	100.0	196	6 ABU70816	Abu70816 Human adi
11	73	100.0	274	6 ABU70549	Abu70549 Human adi
12	73	100.0	294	7 ADI63068	Adi63068 Human apo
13	73	100.0	332	7 ADI63011	Adi63011 Human apo
14	73	100.0	334	6 ABP98860	Abp98860 Human str
15	73	100.0	342	7 ADM05323	Adm05323 Human pro
16	73	100.0	374	3 AAB12985	Aab12985 Human bet
17	73	100.0	375	1 AAP61532	Aap61532 Sequence
18	73	100.0	375	2 AAR50328	Aar50328 Drug resi
19	73	100.0	375	3 AAB15017	Aab15017 Posttrans
20	73	100.0	375	3 AAY94569	Aay94569 Human car
21	73	100.0	375	3 AAB15016	Aab15016 Posttrans
22	73	100.0	375	5 ABB77395	Abb77395 Human act
23	73	100.0	375	6 ABR64271	Abr64271 Angiogene
24	73	100.0	375	6 ABM04830	Abm04830 Rat cytop
25	73	100.0	375	7 ADB85212	Adb85212 Rat actin

ALIGNMENTS

RESULT 1

AAW92539
ID AAW92539 standard; peptide; 15 AA.

XX AC AAW92539;

XX DT 26-APR-1999 (first entry)

XX DE Beta-actin reference peptide substrate #13.

XX KW Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity.

XX OS Synthetic.

XX PN WO9853322-A1.

XX PD 26-NOV-1998.

XX PF 22-MAY-1998; 98WO-GB001485.

XX PR 23-MAY-1997; 97GB-00010762.

XX PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

XX PI Willison K, Hynes G, Liou AK;

XX DR WPI; 1999-070162/06.

XX PT Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

XX PS Disclosure; Fig 10; 97pp; English.

XX CC This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

Ad611174 Rat Prote
Adf30525 Rat angio
Adi63062 Human apo
Adi62970 Human apo
Adi63040 Human apo
Adi13002 Human ste
Adi78489 Actin pro
Adi14103 Human ear
Adp04899 Sea squir
Adp12391 Protein e
Adq26098 Gamma 1 a
Abo84772 Human can
Abm08941 Tumour-as
Adn23274 Bacterial
Adn23274 Amino aci
Adn8828 Amino aci
Adn8825 Amino aci
Adn8826 Amino aci
Adn8827 Amino aci
Aaw19799 Gamma-bmo
Abb58162 Drosophil

CC agents may target cells that are actively synthesising tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AAM92527-W92541 are
 CC peptide substrates used in the method of the invention
 XX
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 73; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
 |||||
 Db 1 ASSSSLEKSYELPDG 15
 |||||

RESULT 2
 AAM80875
 ID AAM80875 standard; protein; 147 AA.
 XX
 AC
 XX
 XX
 DT 13-NOV-2001 (first entry)
 XX
 XX
 DE Human haematological malignancy-related antigen #573.
 XX
 XX
 KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX
 OS Homo sapiens.
 XX
 FN WO200164886-A2.
 XX
 XX
 PD 07-SEP-2001.
 XX
 XX
 PF 01-MAR-2001; 2001WO-US007272.
 XX
 XX
 PR 01-MAR-2000; 2000US-0186126P.
 PR 17-MAR-2000; 2000US-0190479P.
 PR 27-APR-2000; 2000US-0200545P.
 PR 28-APR-2000; 2000US-0200303P.
 PR 28-APR-2000; 2000US-0200779P.
 PR 01-MAY-2000; 2000US-0200999P.
 PR 04-MAY-2000; 2000US-0202084P.
 PR 22-MAY-2000; 2000US-0206201P.
 PR 14-JUL-2000; 2000US-0218950P.
 PR 03-AUG-2000; 2000US-0222903P.
 PR 04-AUG-2000; 2000US-0223416P.
 PR 07-AUG-2000; 2000US-0223378P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX
 PI Gaiger A, Algate PA, Mannion J;
 XX
 XX
 DR WPI; 2001-514842/56.
 XX
 XX
 PT Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX
 XX
 PS Claim 1; Page 743-744; 1252pp; English.
 XX
 XX
 CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B

CC cell non-Hodgkin's lymphoma
 XX
 SQ Sequence 147 AA;

Query Match 100.0%; Score 73; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
 |||||
 Db 3 ASSSSLEKSYELPDG 17
 |||||

RESULT 3
 AAM81886
 ID AAM81886 standard; protein; 147 AA.
 XX
 AC AAM81886;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 XX
 DE Human haematological malignancy-related antigen #1584.
 XX
 XX
 KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX
 OS Homo sapiens.
 XX
 FN WO200164886-A2.
 XX
 XX
 PD 07-SEP-2001.
 XX
 XX
 PF 01-MAR-2001; 2001WO-US007272.
 XX
 XX
 PR 01-MAR-2000; 2000US-0186126P.
 PR 17-MAR-2000; 2000US-0190479P.
 PR 27-APR-2000; 2000US-0200545P.
 PR 28-APR-2000; 2000US-0200303P.
 PR 28-APR-2000; 2000US-0200779P.
 PR 01-MAY-2000; 2000US-0200999P.
 PR 04-MAY-2000; 2000US-0202084P.
 PR 22-MAY-2000; 2000US-0206201P.
 PR 14-JUL-2000; 2000US-0218950P.
 PR 03-AUG-2000; 2000US-0222903P.
 PR 04-AUG-2000; 2000US-0223416P.
 PR 07-AUG-2000; 2000US-0223378P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX
 PI Gaiger A, Algate PA, Mannion J;
 XX
 XX
 DR WPI; 2001-514842/56.
 XX
 XX
 PT Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX
 XX
 PS Claim 1; Page 1141; 1252pp; English.
 XX
 XX
 CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma
 XX
 SQ Sequence 147 AA;

Query Match 100.0%; Score 73; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSLEKSYELPDG 15
|||||
DB 3 ASSSLEKSYELPDG 17
|||||

RESULT 4
AAM81332
ID AAM81332 standard; protein; 147 AA.

XX AC AAM81332;

XX DT 13-NOV-2001 (first entry)

XX DE Human haematological malignancy-related antigen #1030.

XX KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;

XX KW haematological malignancy; antigen; chronic lymphocytic leukaemia;

XX KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

XX OS Homo sapiens.

XX PN WO200164886-A2.

XX PD 07-SEP-2001.

XX PF 01-MAR-2001; 2001WO-US007272.

XX PR 01-MAR-2000; 2000US-0186126P.

XX PR 17-MAR-2000; 2000US-0190479P.

XX PR 27-APR-2000; 2000US-0200545P.

XX PR 28-APR-2000; 2000US-0200303P.

XX PR 28-APR-2000; 2000US-0200779P.

XX PR 01-MAY-2000; 2000US-0200999P.

XX PR 04-MAY-2000; 2000US-0202084P.

XX PR 22-MAY-2000; 2000US-0206201P.

XX PR 14-JUL-2000; 2000US-0218950P.

XX PR 03-AUG-2000; 2000US-0222903P.

XX PR 04-AUG-2000; 2000US-0223416P.

XX PR 07-AUG-2000; 2000US-0223378P.

XX PA (CORI-) CORIXA CORP.

XX PI Gaiger A, Algate PA, Mannion J;

XX PS WPI; 2001-514842/56.

XX PT Compositions and methods for the detection of hematological malignancies,

XX PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and

XX PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.

XX PS Claim 1; Page 925; 1252pp; English.

XX CC The present invention relates to compositions and methods for the

XX CC detection, diagnosis and therapy of hematological malignancies. The

XX CC present sequence is the protein sequence of a human haematological

XX CC malignancy related antigen. The methods of the present invention comprise

XX CC detecting the presence of haematological malignancy related antigen(s) in

XX CC a sample obtained from the patient (an increased level of the

XX CC polypeptide, compared to an unaffected individual, is indicative of an

XX CC increased risk). Haematological malignancies which can be treated using

XX CC the present invention are chronic lymphocytic leukaemia, lymphoma,

XX CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B

XX CC cell non-Hodgkin's lymphoma

XX SQ Sequence 147 AA;

Query Match 100.0%; Score 73; DB 4; Length 147;

Best Local Similarity 100.0%; Pred. No. 6.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSLEKSYELPDG 15

|||||

DB 3 ASSSLEKSYELPDG 17

|||||

RESULT 5

ABO84771

ID ABO84771 standard; protein; 149 AA.

XX AC ABO84771;

XX DT 18-NOV-2004 (first entry)

XX DE Human cancer-associated protein (CAP) HP07-010.

XX KW Human; cancer-associated protein; CAP; cancer; cytostatic.

XX OS Homo sapiens.

XX PN WO2004058146-A2.

XX PD 15-JUL-2004.

XX PF 15-DEC-2003; 2003WO-US040081.

XX PR 17-DEC-2002; 2002US-00322281.

XX PA (SAGR-) SAGRES DISCOVERY INC.

XX PI Morris DW, Malandro MS;

XX DR WPI; 2004-499109/47.

XX DR N-PSDB; ABD33111.

XX PT Novel human cancer associated protein encoded within open reading frame

XX PT of cancer associated gene, useful as targets for diagnosing cancer.

XX PS Claim 18; SEQ ID NO 66; 182pp; English.

XX CC The invention relates to cancer-associated proteins (CAP) and the cancer-

XX CC associated (CA) nucleic acids encoding them. The invention also relates

XX CC to a method for treating cancers involving administering to a patient an

XX CC inhibitor of CAP, and a method of screening for anticancer activity in a

XX CC potential drug involving providing a cell that expresses a CA gene,

XX CC contacting a tissue sample derived from a cancer cell with an anticancer

XX CC drug candidate and monitoring the effect of the anticancer drug candidate

XX CC on expression of the CA gene. The CAP proteins are useful for detecting

XX CC cancer associated with expression of a CAP protein in a test cell sample

XX CC and for screening for a bioactive agent capable of modulating the

XX CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing

XX CC cancer, involving determining the expression of a CA nucleic acid in a

XX CC tissue. This sequence represents a human CAP of the invention. Note: The

XX CC sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 149 AA;

Query Match 100.0%; Score 73; DB 8; Length 149;

Best Local Similarity 100.0%; Pred. No. 6.9e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSLEKSYELPDG 15

|||||

DB 5 ASSSLEKSYELPDG 19

|||||

RESULT 6

ABG15497

ID ABG15497 standard; protein; 153 AA.

XX

AC ABG15497;
 XX 18-FEB-2002 (first entry)
 DT DE
 XX Novel human diagnostic protein #15488.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US008631.
 PF 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI: 2001-639362/73.
 DR N-PSDB; AAS79684.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 45856; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 153 AA;
 SQ Query Match 100.0%; Score 73; DB 4; Length 153;
 Best Local Similarity 100.0%; Pred. NO. 7.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASSSSLEKSYELPDG 15
 |||||
 Db 72 ASSSSLEKSYELPDG 86
 |||||
 RESULT 7
 ABP42724
 ID ABP42724 standard; protein; 157 AA.
 XX
 AC ABP42724;
 XX
 DT 22-AUG-2002 (first entry)
 DE Human ovarian antigen HOVCV33, SEQ ID NO:3856.
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX Homo sapiens.
 OS WO200200677-A1.
 PN 03-JAN-2002.
 PD 07-JUN-2001; 2001WO-US018569.
 PF 07-JUN-2000; 2000US-0209467P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Birse CE, Rosen CA;
 PI WPI: 2002-147878/19.
 DR N-PSDB; ABQ55801.
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX Claim 11; SEQ ID NO 3856; 2922pp; English.
 PS The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompassing polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 157 AA;
 SQ Query Match 100.0%; Score 73; DB 5; Length 157;
 Best Local Similarity 100.0%; Pred. NO. 7.4e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSLEKSYELPDG 15
|||||
Db 12 ASSSLEKSYELPDG 26
|||||

RESULT 8
ABP42912
ID ABP42912 standard; protein; 168 AA.
XX ABP42912;
AC ABP42912;
CC ABP42912;
DT 22-AUG-2002 (first entry)
XX Human ovarian antigen HPDQ265, SEQ ID NO:4044.
DE Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX Homo sapiens.
OS Homo sapiens.
XX WO200200677-A1.
PN WO200200677-A1.
XX 03-JAN-2002.
PD 03-JAN-2002.
XX 07-JUN-2001; 2001WO-US018569.
PF 07-JUN-2001; 2001WO-US018569.
XX 07-JUN-2000; 2000US-0209467P.
PR 07-JUN-2000; 2000US-0209467P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
PI Birse CE, Rosen CA;
DR WPI; 2002-147878/19.
N-PSDB; ABQ55989.
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX Claim 11; SEQ ID NO 4044; 2922pp; English.

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may

CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 168 AA;
SQ Sequence 168 AA;

Query Match 100.0%; Score 73; DB 5; Length 168;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSLEKSYELPDG 15
|||||
Db 117 ASSSLEKSYELPDG 131
|||||

RESULT 9
ABU70840
ID ABU70840 standard; protein; 185 AA.
XX ABU70840;
AC ABU70840;
CC ABU70840;
DT 10-JUN-2003 (first entry)
XX 10-JUN-2003 (first entry)
DE Human adipocyte Selected Interacting domain, SID, #471.
XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;
KW antidiabetic; protein-protein interaction; diabetes;
KW yeast 2-hybrid assay; metabolic disorder; obesity.
XX Homo sapiens.
OS Homo sapiens.
XX WO200286122-A2.
PN WO200286122-A2.
XX 31-OCT-2002.
PD 31-OCT-2002.
XX 14-MAR-2002; 2002WO-EP003768.
PF 14-MAR-2002; 2002WO-EP003768.
PR 14-MAR-2001; 2001US-0275734P.
XX (HYBR-) HYBRIGENICS.
PA (HYBR-) HYBRIGENICS.
XX Legrain P, Daviet L;
PI Legrain P, Daviet L;
XX WPI; 2003-103412/09.
DR WPI; 2003-103412/09.
N-PSDB; ACA57384.
XX New complex between two interacting proteins in adipocyte cells, useful
PT for identifying selected interacting domains that modulate protein
PT interactions, or for preventing or treating metabolic disorders such as
PT obesity or diabetes.
XX Claim 6; Page 266; 382pp; English.

CC The invention relates to a complex between two interacting proteins in
CC adipocyte cells, given in the specification. The proteins are identified
CC by selecting a bait protein from a known adipocyte marker and then
CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
CC members of an adipocyte cDNA library. The proteins are designated SID
CC (RTM) (selected interacting domains) proteins. Also included are a
CC polynucleotide encoding a polypeptide in the adipocyte cells, a
CC recombinant host cell expressing at least one of the interacting
CC polypeptides of the complex, selecting a modulating compound in adipocyte
CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
CC sequences given in the specification (including its fragment or variant),
CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
CC given in the specification (including its fragment or variant), a vector
CC comprising the SID (RTM) polynucleotide, a recombinant host cell
CC comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.
 CC The complex, polypeptides, polynucleotides and compounds are useful for
 CC preventing or treating metabolic disorders such as obesity or diabetes.
 CC The polynucleotides are useful as probes or primers. The complex is
 CC particularly useful for identifying selected interacting domains (SID
 CC (RTM)) for screening drugs that modulate the protein interaction, thus
 CC exhibiting the therapeutic effect. The present sequence represents a SID
 CC (prey) protein of the invention
 CC XX
 CC SQ Sequence 196 AA;
 Query Match 100.0%; Score 73; DB 6; Length 196;
 Best Local Similarity 100.0%; Pred. No. 9.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASSSLSLEKSYELPDG 15
 DB 105 ASSSLSLEKSYELPDG 119
 RESULT 11
 ABU70549
 ID ABU70549 standard; protein; 274 AA.
 AC ABU70549;
 XX
 DT 10-JUN-2003 (first entry)
 DE Human adipocyte Selected Interacting domain, SID, #180.
 XX
 KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 KW antidiabetic; protein-protein interaction; diabetes;
 KW yeast 2-hybrid assay; metabolic disorder; obesity.
 XX
 OS Homo sapiens.
 XX
 PN WO200286122-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 14-MAR-2002; 2002WO-EP003768.
 XX
 PR 14-MAR-2001; 2001US-0275734P.
 XX
 PA (HYBR-) HYBRIGENICS.
 XX
 PI Legrain P, Daviet L;
 XX
 DR WPI; 2003-103412/09.
 DR N-PSDB; ACAS7093.
 XX
 PT New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 PT obesity or diabetes.
 XX
 PS Claim 6; Page 167; 382pp; English.
 XX
 CC The invention relates to a complex between two interacting proteins in
 CC adipocyte cells, given in the specification. The proteins are identified
 CC by selecting a bait protein from a known adipocyte marker and then
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 CC members of an adipocyte cDNA library. The proteins are designated SID
 CC (RTM) (selected interacting domains) proteins. Also included are a
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a
 CC recombinant host cell expressing at least one of the interacting
 CC polypeptides of the complex, selecting a modulating compound in adipocyte
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
 CC sequences given in the specification (including its fragment or variant),
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
 CC given in the specification (including its fragment or variant), a vector
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell
 CC comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.
 CC The complex, polypeptides, polynucleotides and compounds are useful for
 CC preventing or treating metabolic disorders such as obesity or diabetes.
 CC The polynucleotides are useful as probes or primers. The complex is
 CC particularly useful for identifying selected interacting domains (SID
 CC (RTM)) for screening drugs that modulate the protein interaction, thus
 CC exhibiting the therapeutic effect. The present sequence represents a SID
 CC (prey) protein of the invention
 CC XX
 CC SQ Sequence 185 AA;
 Query Match 100.0%; Score 73; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 8.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASSSLSLEKSYELPDG 15
 DB 115 ASSSLSLEKSYELPDG 129
 RESULT 10
 ABU70816
 ID ABU70816 standard; protein; 196 AA.
 AC ABU70816;
 XX
 DT 10-JUN-2003 (first entry)
 DE Human adipocyte Selected Interacting domain, SID, #447.
 XX
 KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 KW antidiabetic; protein-protein interaction; diabetes;
 KW yeast 2-hybrid assay; metabolic disorder; obesity.
 XX
 OS Homo sapiens.
 XX
 PN WO200286122-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 14-MAR-2002; 2002WO-EP003768.
 XX
 PR 14-MAR-2001; 2001US-0275734P.
 XX
 PA (HYBR-) HYBRIGENICS.
 XX
 PI Legrain P, Daviet L;
 XX
 DR WPI; 2003-103412/09.
 DR N-PSDB; ACAS7360.
 XX
 PT New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 PT obesity or diabetes.
 XX
 PS Claim 6; Page 259-260; 382pp; English.
 XX
 CC The invention relates to a complex between two interacting proteins in
 CC adipocyte cells, given in the specification. The proteins are identified
 CC by selecting a bait protein from a known adipocyte marker and then
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 CC members of an adipocyte cDNA library. The proteins are designated SID
 CC (RTM) (selected interacting domains) proteins. Also included are a
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a
 CC recombinant host cell expressing at least one of the interacting
 CC polypeptides of the complex, selecting a modulating compound in adipocyte
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
 CC sequences given in the specification (including its fragment or variant),
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
 CC given in the specification (including its fragment or variant), a vector
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell
 CC comprising the vector, a protein chip comprising the polypeptides and a

CC extracts), encoded polypeptide (or their receptors) and/or agents that
CC inhibit their activity (including antisense sequences) are used for
CC treatment or prevention of tumours, autoimmune or degenerative diseases
CC and viral infections, specifically leukaemia, carcinoma, sarcoma,
CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection
CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or
CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver
CC disease. Detection of the polynucleotides and derived polypeptides can
CC also be used for diagnosis of these diseases. This sequence represents an
CC apoptosis-associated protein described in the invention.

XX SQ Sequence 332 AA;
Query Match 100.0%; Score 73; DB 7; Length 332;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSLEKSYELPDG 15
DB 188 ASSSLEKSYELPDG 202
RESULT 14
ABP98860
ID ABP98860 standard; protein; 334 AA.
XX AC ABP98860;
XX DT 15-JUL-2003 (first entry)
XX DE Human structural and cytoskeletal associated protein #51.

XX KW Cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; antianginal;
KW neuroprotective; cerebroprotective; hypotensive; cardiant; osteopathic;
KW antiinflammatory; antiarthritic; virucide; gene therapy; human; stroke;
KW structural and cytoskeleton-associated protein; SCAP; cancer; angina;
KW atherosclerosis; epilepsy; Huntington's disease; hypertension;
KW heart failure; osteoporosis; osteoarthritis.
XX OS Homo sapiens.
XX WO2003031940-A2.
XX PD 17-APR-2003.
XX PF 10-OCT-2002; 2002WO-US032851.
XX PR 12-OCT-2001; 2001US-0328931P.
XX PR 19-OCT-2001; 2001US-0360681P.
XX PR 02-NOV-2001; 2001US-0343896P.
XX PR 09-NOV-2001; 2001US-0346308P.
XX PR 16-NOV-2001; 2001US-0332385P.
XX PR 07-DEC-2001; 2001US-0340776P.
XX PR 11-JAN-2002; 2002US-0347703P.

XX PA (INCY-) INCYTE GENOMICS INC.
XX XX Becha SD, Bhatia U, Blake JJ, Borowsky ML, Burrill JD, Chang H;
PI Chawla NK, Elliott VS, Emerling EM, Forsythe IJ, Gorvad AE;
PI Griffin JA, Hafalia AJA, Ho A, Ison CH, Kabie AE, Khare R, Lal PG;
PI Lee S, Lee EA, Lee SY, Lehr-Nason PM, Li JX, Lindquist EA, Luo W;
PI Marquis JP, Ramkumar J, Richardson TW, Sprague WM, Swarnakar A;
PI Tang YT, Warren BA, Yang J, Yue H, Zebartjadian Y, Zheng W;
XX WPI; 2003-403125/38.
XX DR N-PSDB; ACC44347.

XX XX New human structural and cytoskeleton-associated proteins (SCAP) useful
PT for diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant SCAP expression e.g. cancer, osteoporosis, or epilepsy.
XX Claim 1; Page 310; 361pp; English.

CC This sequence represents a novel isolated human structural and
CC cytoskeleton-associated protein (SCAP) polypeptide. The polypeptides and
CC polynucleotides encoding them are useful in diagnosing, treating and
CC preventing diseases or conditions associated with the decreased
CC expression or over expression of SCAP, such as cell proliferative (e.g.
CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's
CC disease, stroke), heart (e.g. hypertension, heart failure, angina) and
CC skeletal muscle disorders (e.g. osteoporosis, osteoarthritis) or viral
CC infections. These are also useful in assessing the effects of exogenous
CC compounds on the expression of nucleic acid and amino acid sequences of
CC SCAP. The SCAP or its fragments are useful in screening compounds for
CC effectiveness as agonist or antagonist of the polypeptides, or in
CC altering the expression of the target polynucleotide and compounds that
CC specifically bind to or modulate the activity of the polypeptide. The
CC microarray is useful in monitoring or measuring protein-protein
CC interactions, drug-target interactions, and gene expression profiles
XX SQ Sequence 334 AA;

Query Match 100.0%; Score 73; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSLEKSYELPDG 15
DB 190 ASSSLEKSYELPDG 204
RESULT 15
ADM05323
ID ADM05323 standard; protein; 342 AA.
XX AC ADM05323;
XX DT 20-MAY-2004 (first entry)
XX DE Human protein of the invention SEQ ID NO:4008.
XX KW human; gene therapy; diagnostic marker; pharmaceutical.

XX OS Homo sapiens.
XX EP1347046-A1.
XX PD 24-SEP-2003.
XX PF 12-APR-2002; 2002EP-00008400.
XX PR 22-MAR-2002; 2002JP-00137785.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-723558/69.
XX DR N-PSDB; ADM02880.

XX XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX Claim 1; SEQ ID NO 4008; 305pp; English.
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.

XX
 SQ Sequence 342 AA;

Query Match 100.0%; Score 73; DB 7; Length 342;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
 |||||
 Db 198 ASSSSLEKSYELPDG 212

Search completed: April 8, 2005, 10:50:49
 Job time : 62.4 sec

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-13
Perfect score: 73
Sequence: 1 ASSSSLEKSYELPDG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	239	4	US-09-949-016-10409
2	73	100.0	374	3	US-08-609-236-6
3	73	100.0	375	3	US-09-106-217-16
4	73	100.0	375	4	US-09-976-594-731
5	73	100.0	376	1	US-08-588-113-2
6	73	100.0	376	4	US-09-949-016-6100
7	73	100.0	377	3	US-09-106-217-2
8	73	100.0	377	4	US-09-919-172-33
9	73	100.0	377	4	US-09-917-254-53
10	73	100.0	386	4	US-09-949-016-7721
11	73	100.0	399	4	US-09-949-016-9424
12	73	100.0	402	4	US-09-949-016-10757
13	73	100.0	404	4	US-09-949-016-11313
14	69	94.5	371	3	US-08-261-206A-77
15	69	94.5	375	1	US-09-171-337A-8
16	69	94.5	375	3	US-09-631-022-8
17	66	90.4	375	3	US-09-171-337A-7
18	66	90.4	375	4	US-09-631-022-7
19	65	89.0	375	2	US-08-494-151-14
20	61	83.6	377	4	US-09-248-796A-14109
21	55.5	76.0	146	3	US-09-306-446C-5
22	55.5	76.0	374	3	US-09-306-446C-2
23	40	54.8	327	4	US-09-533-029-68
24	40	54.8	397	4	US-09-248-796A-18243
25	40	54.8	872	4	US-09-543-681A-5785
26	39	53.4	16	4	US-09-786-066-1
27	39	53.4	16	4	US-09-786-066-6

28	39	53.4	16	4	US-09-835-072-7	Sequence 7, Appli
29	39	53.4	103	3	US-08-894-173-77	Sequence 77, Appl
30	39	53.4	103	3	US-09-398-193-77	Sequence 77, Appl
31	39	53.4	114	3	US-08-894-173-97	Sequence 97, Appl
32	39	53.4	114	3	US-09-398-193-97	Sequence 97, Appl
33	39	53.4	168	4	US-09-949-016-8494	Sequence 8494, Ap
34	39	53.4	182	4	US-09-543-681A-5698	Sequence 5698, Ap
35	39	53.4	434	4	US-09-270-767-41796	Sequence 41796, A
36	39	53.4	479	4	US-09-248-796A-17040	Sequence 17040, A
37	39	53.4	479	4	US-09-248-796A-17041	Sequence 17041, A
38	39	53.4	741	4	US-09-252-991A-22440	Sequence 22440, A
39	39	53.4	1099	3	US-08-726-214-14	Sequence 14, Appl
40	38	52.1	103	3	US-08-894-173-78	Sequence 78, Appl
41	38	52.1	103	3	US-09-398-193-78	Sequence 78, Appl
42	38	52.1	123	4	US-09-270-767-59148	Sequence 59148, A
43	38	52.1	235	3	US-09-066-408-12	Sequence 12, Appl
44	38	52.1	359	4	US-09-270-767-43751	Sequence 43751, A
45	38	52.1	469	4	US-09-489-039A-10214	Sequence 10214, A

ALIGNMENTS

RESULT 1
US-09-949-016-10409
; Sequence 10409, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10409
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10409

Query Match 100.0%; Score 73; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
Db 95 ASSSSLEKSYELPDG 109

RESULT 2
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398e1 Sickie Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; DESCRIPTION:
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
;
US-08-609-236-6
;
Query Match 100.0%; Score 73; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
Db 230 ASSSSLEKSYELPDG 244

RESULT 3
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Rothwell, Figs, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217

; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; DESCRIPTION:
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
;
US-08-609-236-6
;
Query Match 100.0%; Score 73; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
Db 230 ASSSSLEKSYELPDG 244

RESULT 3
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Rothwell, Figs, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217

; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-106-217-16
;
Query Match 100.0%; Score 73; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
Db 231 ASSSSLEKSYELPDG 245

RESULT 4
US-09-976-594-731
; Sequence 731, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 731
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
;
US-09-976-594-731
;
Query Match 100.0%; Score 73; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
Db 231 ASSSSLEKSYELPDG 245

RESULT 5
US-08-588-113-2
; Sequence 2, Application US/08588113
; Patent No. 5710003
; GENERAL INFORMATION:
; APPLICANT: McHugh, Kirk M.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5710003ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
```



```

; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,113
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: TJU-1652
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-588-113-2

Query Match 100.0%; Score 73; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
| | | | | | | | | | | | | | | |
DB 232 ASSSSLEKSYELPDG 246

RESULT 6
US-09-949-016-6100
; Sequence 6100, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6100
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6100

Query Match 100.0%; Score 73; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
| | | | | | | | | | | | | | | |
DB 232 ASSSSLEKSYELPDG 246

RESULT 7
US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; CARDIOMYOPATHY, A HERITABLE FORM OF HEART FAILURE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Earnat & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-106-217-2

Query Match 100.0%; Score 73; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASSSSLEKSYELPDG 15
| | | | | | | | | | | | | | | |
DB 233 ASSSSLEKSYELPDG 247

RESULT 8
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
; US-09-919-172-33

Query Match 100.0%; Score 73; DB 4; Length 377;
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Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSLEKSYELPDG 15
|||||
Db 233 ASSSLEKSYELPDG 247

RESULT 9

US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224 (JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 100.0%; Score 73; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSLEKSYELPDG 15
|||||
Db 233 ASSSLEKSYELPDG 247

RESULT 10

US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

Query Match 100.0%; Score 73; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSLEKSYELPDG 15
|||||
Db 242 ASSSLEKSYELPDG 256

RESULT 11

US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 73; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSLEKSYELPDG 15
|||||
Db 255 ASSSLEKSYELPDG 269

RESULT 12

US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match 100.0%; Score 73; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASSSLEKSYELPDG 15
|||||
Db 258 ASSSLEKSYELPDG 272

RESULT 13

US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

```

; MOLECULE TYPE: protein
; US-08-261-206A-77

Query Match          94.5%; Score 69; DB 1; Length 371;
Best Local Similarity 93.3%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 1; Indels 0; G

QY 1 ASSSSLEKSYELPDG 15
   | | | | | | | | | |
Db 229 AQSSSLEKSYELPDG 243

RESULT 15
US-09-171-337A-8
; Sequence 8, Application US/09171337A
; Patent No. 6300095
; GENERAL INFORMATION:
; APPLICANT: BARREDO FUENTE, Jose Luis
; RODRIGUEZ SAIZ, Marta
; COLLADOS DE LA VIEJA, Alfonso J.
; MORENO VALLE,Miguel Angel
; SALTO MALDONADO, Francisco
; DIEZ GARCIA, BRUNO
; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
; AND -ACTIN AND THEIR USE IN FILAMENTOUS
; FUNGI EXPRESSION, SECRETION AND ANTISENSE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61 STREET
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/4" Disk 1.44MB
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
; SOFTWARE: WordPerfect 8 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,337A
; FILING DATE: 14-May-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ES98/00056
; FILING DATE: 5-MAR-1998
; APPLICATION NUMBER: ES9700482
; FILING DATE: 5-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford J.
; REGISTRATION NUMBER: 30,086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 232288
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; ORIGINAL SOURCE:
; ORGANISM: Acremonium chrysogenum
; FEATURE:
; OTHER INFORMATION: amino acid sequence of the -actin
; protein with a molecular weight of
; 41612 Da.
; SEQUENCE DESCRIPTION: SEQ ID NO: 8

US-09-171-337A-8

Query Match          94.5%; Score 69; DB 3; Length 375;
Best Local Similarity 93.3%; Pred. No. 0.00016;

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us-09-423-351c-13.ra1

Fri Apr 8 14:14:19 2005

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASSSSLEKSYELPDG 15
| | | | | | | | | | | | | | |
Db 231 AQSSSLEKSYELPDG 245

Search completed: April 8, 2005, 12:07:39
Job time : 17.5333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: April 8, 2005, 09:58:56 ; Search time 9.3333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-11
Perfect score: 75
Sequence: 1 KILTERGYSTTTAE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	195	2 S20097	actin 85c - potato (fragment)
2	75	100.0	328	2 S05430	actin beta - grass carp
3	75	100.0	336	2 T04085	actin - maize (fra
4	75	100.0	362	2 A26559	actin type 5, cyto
5	75	100.0	365	2 S49007	actin - Pythium ir
6	75	100.0	370	2 A29664	actin - sea urchin
7	75	100.0	374	1 ATBOB	actin beta - bovin
8	75	100.0	374	1 ATBOG	actin gamma - bovi
9	75	100.0	374	2 JC5818	gamma-actin - huma
10	75	100.0	375	1 ATRTC	actin beta - rat
11	75	100.0	375	1 A48324	actin beta, cytosk
12	75	100.0	375	1 ATAX	actin - Acanthamo
13	75	100.0	375	1 ATCHB	actin beta - chick
14	75	100.0	375	1 ATDO	actin - slime mold
15	75	100.0	375	1 ATHUB	actin beta - human
16	75	100.0	375	1 ATHUG	actin gamma 1 - hu
17	75	100.0	375	1 ATWSB	actin beta - mouse
18	75	100.0	375	1 ATWSG	actin gamma - mous
19	75	100.0	375	1 ATBBB	actin beta, non-mu
20	75	100.0	375	1 S11222	actin gamma, cytos
21	75	100.0	375	1 ATUN	actin - Phytophtho
22	75	100.0	375	2 S33386	actin, cytosolic (
23	75	100.0	375	2 JE0415	actin B - Phytoph
24	75	100.0	375	2 S71125	actin beta-2, cyto
25	75	100.0	375	2 S71124	actin beta-1, cyto
26	75	100.0	375	2 S71126	actin beta, cytosol
27	75	100.0	375	2 A55001	actin beta - goose
28	75	100.0	376	1 ATFF7	actin 7 - fruit fl
29	75	100.0	376	1 A43552	actin gamma, cytos

30	75	100.0	376	1 ATFY	actin - slime mold
31	75	100.0	376	1 ATRZ3	actin 3 - rice
32	75	100.0	376	1 ATRZ7	actin 7 - rice
33	75	100.0	376	1 ATURS	actin Cyl - sea ur
34	75	100.0	376	2 B23412	actin 12 - slime m
35	75	100.0	376	2 A48449	Actin-1A - nematod
36	75	100.0	376	2 S04538	actin 87E - fruit
37	75	100.0	376	2 JC1246	actin - fruit fly
38	75	100.0	376	2 JS0189	actin, cytosolic -
39	75	100.0	376	2 JS0190	actin, muscle - st
40	75	100.0	376	2 S07288	actin 15A - sea ur
41	75	100.0	376	2 S09578	actin - sea urchin
42	75	100.0	376	2 C23412	actin 3-sub1 - eli
43	75	100.0	376	2 A25084	actin 15 - slime m
44	75	100.0	376	2 J00154	actin - Hydra atte
45	75	100.0	376	2 JN0832	actin (clone gens)

ALIGNMENTS

RESULT 1

S20097
actin 85c - potato (fragment)
C:Species: Solanum tuberosum (potato)
C:Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C:Accession: S20097
R:Drouin, G.; Dover, G.A.
J. Mol. Evol. 31, 132-150, 1990
A:Title: Independent gene evolution in the potato actin gene family demonstrated by phylogenetic analysis
A:Reference number: S20092; MUID:91012599; PMID:2120451
A:Accession: S20097
A:Molecule type: DNA
A:Residues: 1-195 <DRO>
A:Cross-references: UNIPROT:P30170; EMBL:X55747; NID:G21541; PIDN:CAA39277.1; PID:gl34553
C:Genetics:
A:Introns: 132/1
C:Superfamily: actin
C:Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 75; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSTTTAE 15
Db 173 KILTERGYSTTTAE 187

RESULT 2

S05430
actin beta - grass carp
C:Species: Ctenopharyngodon idella (grass carp)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S05430
R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.
Nucleic Acids Res. 17, 5850, 1989
A:Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A:Reference number: S05430; MUID:89345185; PMID:2762162
A:Accession: S05430
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-328 <LIU>
A:Cross-references: UNIPROT:P83751; EMBL:M25013
C:Genetics:
A:Introns: 41/3; 121/3; 268/1
C:Superfamily: actin
C:Keywords: cytoskeleton; methylated amino acid
F,7/3/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Apr 8 14:14:17 2005

us-09-423-351c-11.rpr

QY 1 KILTERGYSTTTAE 15
| | | | | | | | | | | | | | |
Db 191 KILTERGYSTTTAE 205

RESULT 3
T04085
actin - maize (fragment)
C/Species: Zea mays (maize)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T04085
R/de Sa, M.; Drouin, G.
Mol. Biol. Evol. 13, 1198-1212, 1996
A/Title: Phylogeny and substitution rates of angiosperm actin genes.
A/Reference number: Z15197; MUID:97051711; PMID:8896372
A/Accession: T04085
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-336 <DES>
A/Cross-references: UNIPROT:P93638; EMBL:U60513; NID:g1490392; PIDN:AB40107.1; PID:g149
C/Genetics:
A/Genes: Maz63
A/Note: Intron positions not resolved (incomplete sequence)
C/Superfamily: actin
C/Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 75; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.5e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 KILTERGYSTTTAE 15
| | | | | | | | | | | | | | |
Db 173 KILTERGYSTTTAE 187

RESULT 4
A26559
actin type 5, cytosolic - chicken
C/Species: Gallus gallus (chicken)
C/Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C/Accession: A26559
R/Bergema, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A/Reference number: A26559; MUID:85213487; PMID:4000121
A/Accession: A26559
A/Molecule type: DNA
A/Residues: 1-362 <BER>
C/Superfamily: actin
C/Keywords: cytosol; methylated amino acid
F/74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.8e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 KILTERGYSTTTAE 15
| | | | | | | | | | | | | | |
Db 192 KILTERGYSTTTAE 206

RESULT 5
S49007
actin - Pythium irregulare (fragment)
C/Species: Pythium irregulare
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
C/Accession: S49007
R/Bhattacharya, D.; Stickel, S.K.
J. Mol. Evol. 39, 56-61, 1994
A/Title: Sequence analysis of duplicated actin genes in Lagenidium giganteum and Pythium
A/Reference number: S49007; MUID:94343543; PMID:8064873
A/Accession: S49007
A/Status: translation not shown

A/Molecule type: DNA
A/Residues: 1-365 <BHA>
A/Cross-references: EMBL:X76725
A/Experimental source: strain P3804
C/Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 KILTERGYSTTTAE 15
| | | | | | | | | | | | | | |
Db 181 KILTERGYSTTTAE 195

RESULT 6
A29664
actin - sea urchin (Strongylocentrotus purpuratus)
C/Species: Strongylocentrotus purpuratus (purple urchin)
C/Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
C/Accession: A29664
R/Crain Jr., W.R.; Boshar, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D.
J. Mol. Evol. 25, 37-45, 1987
A/Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with
A/Reference number: A29664; MUID:87311761; PMID:3114500
A/Accession: A29664
A/Molecule type: DNA
A/Residues: 1-370 <CRA>
A/Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
A/Note: the authors translated the codon CAG for residue 260 as Glu
C/Superfamily: actin
C/Keywords: methylated amino acid
F/73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.9e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 KILTERGYSTTTAE 15
| | | | | | | | | | | | | | |
Db 188 KILTERGYSTTTAE 202

RESULT 7
ATB08
actin beta - bovine (tentative sequence)
C/Species: Bos primigenius taurus (cattle)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: E14185; A39105; A02999; A14185
R/Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A/Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A/Reference number: A14185; MUID:79045349; PMID:213279
A/Accession: E14185
A/Molecule type: protein
A/Residues: 1-374 <VAN>
A/Cross-references: UNIPROT:P60712
A/Note: only peptides that differed in composition from the corresponding peptides of ra
R/Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A/Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analysis
A/Reference number: A39105; MUID:84032385; PMID:6195151
A/Accession: A39105
A/Molecule type: mRNA
A/Residues: 76-227;344-374 <DEG>
A/Cross-references: GB:X00623
A/Note: actins beta and gamma were not distinguished in this study
C/Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C/Superfamily: actin
C/Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F/1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F/72/Modified site: 3'-methylhistidine (His) #status predicted

```

Query Match      100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
   |||||
Db 190 KILTERGYSFTTAAE 204

RESULT 8
ATBOG
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: B14185; A02999
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: B14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P02571
A:Note: Only peptides that differed in composition from the corresponding peptides of ra
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
F172/Modified site: 3'-methylhistidine (His) #status predicted

Query Match      100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
   |||||
Db 190 KILTERGYSFTTAAE 204

RESULT 9
JC5818
gamma-actin - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: JC5818; PC4501
R:Hauechilde, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens
Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A:Title: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes
A:Reference number: JC5818; MUID:98096379; PMID:9434766
A:Accession: JC5818
A:Molecule type: protein
A:Residues: 1-374 <HAU>
A:Cross-references: UNIPROT:P02571
A:Experimental source: monocyte
A:Accession: PC4501
A:Molecule type: protein
A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A:Experimental source: monocyte
C:Comment: This protein is involved in a signal transduction that eventually leads to mo
C:Superfamily: actin

Query Match      100.0%; Score 75; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
   |||||
Db 190 KILTERGYSFTTAAE 204

RESULT 10
ATRTC
actin beta - rat

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C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
C:Accession: A38571; A02999
R:Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A:Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A:Reference number: A38571; MUID:83168920; PMID:6300777
A:Accession: A38571
A:Molecule type: DNA
A:Residues: 1-375 <NUD>
A:Cross-references: GB:J00691; NID:G202653; PIDN:AAA40457.1; PID:G202654
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Genetics:
A:Introns: 41/3; 121/3; 268/1; 328/3
C:Superfamily: actin
C:Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;
F:2-375/Product: actin beta #status predicted <MAT>
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match      100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
   |||||
Db 191 KILTERGYSFTTAAE 205

RESULT 11
A48324
actin beta, cytoskeletal - common carp
C:Species: Cyprinus carpio (common carp)
C:Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: A48324
R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
DNA Seq. 1, 125-136, 1990
A:Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A:Reference number: A48324; MUID:92190540; PMID:2134183
A:Accession: A48324
A:Molecule type: DNA
A:Residues: 1-375 <LIU>
A:Cross-references: UNIPROT:P83750; GB:M24113; NID:G2113041; PIDN:AAA6886.1; PID:G213042
A:Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 a
7 as Pro
A:Note: the authors failed to translated the codon GGT for residue 42 as Gly
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Genetics:
A:Introns: 41/3; 121/3; 268/3; 328/3
C:Superfamily: actin
C:Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; m
F:2-375/Product: actin beta, cytoskeletal #status predicted <MAT>
F:2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match      100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
   |||||
Db 191 KILTERGYSFTTAAE 205

RESULT 12
ATAX
actin - Acanthamoeba castellanii
C:Species: Acanthamoeba castellanii
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A92886; A03004
R:Nellen, W.; Gallwitz, D.
J. Mol. Biol. 159, 1-18, 1982
A:Title: Actin genes and actin messenger RNA in Acanthamoeba castellanii. Nucleotide se
A:Reference number: A92886; MUID:83033627; PMID:6290670

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A:Accession: A92886
A:Molecule type: DNA
A:Residues: 1-375 <NEL>
A:Cross-references: UNIPROT:P02578; GB:V00002; GB:J01016; NID:G5565; PIDN:CAA23399.1; PI
C:Comment: There are at least three actin genes in A. castellanii.
C:Genetics:
A:Introns: 105/3
C:Superfamily: actin
C:Keywords: methylated amino acid
F:7/3/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTTAE 15
|||
Db 191 KILTERGYSFTTTAE 205
|||

RESULT 13
ATDO
actin beta - chicken
C:Species: Gallus gallus (chicken)
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A20888; I50154
R:Kost, T.A.; Theodorakis, N.; Hughes, S.H.
Nucleic Acids Res. 11, 8287-8301, 1983
A>Title: The nucleotide sequence of the chick cytoplasmic beta-actin gene.
A:Reference number: A20888; MUID:84169478; PMID:6324080
A:Accession: A20888
A:Molecule type: DNA
A:Residues: 1-375 <KOS>
A:Cross-references: UNIPROT:P60706; EMBL:X00182
A>Note: the sequence shown follows the authors' translation at position 336
R:Chang, K.
Mol. Cell. Biol. 4, 2498-2508, 1984
A>Title: Isolation and characterization of six different chicken actin genes.
A:Reference number: I50153; MUID:85085956; PMID:6513927
A:Accession: I50154
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-17 <CHA>
A:Cross-references: GB:K02259; NID:g211086; PIDN:AAA48572.1; PID:g211087
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Genetics:
A:Introns: 41/3; 121/3; 268/1; 328/3
C:Superfamily: actin
C:Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F:2-375/Product: actin beta #status predicted <MAR>
F:2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F:7/3/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTTAE 15
|||
Db 191 KILTERGYSFTTTAE 205
|||

RESULT 14
ATDO
actin - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A93223; A92871; S67999; R03004
R:Vandekerckhove, J.; Weber, K.
Nature 284, 475-477, 1980
A>Title: Vegetative Dictyostelium cells containing 17 actin genes express a single major
A:Reference number: A93223; MUID:80143370; PMID:6892652
A:Accession: A93223

Mol. Cell. Biol. 3, 787-795, 1983
 A:Title: Isolation and characterization of full-length cDNA clones for human alpha-, beta- and gamma-actin.
 A:Reference number: I39394; MUID:83244575; PMID:6865942
 A:Accession: I39394
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-17 <GUN>
 A:Cross-references: GB:K00790; NID:G178031; PIDN:AAA51578.1; PID:G178032
 R:Ohmuri, H.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S38782
 A:Accession: S38782
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-138, 'M', 140-294, 'D', 296-375 <OHM>
 A:Cross-references: EMBL:X63432; NID:G28335; PIDN:CAA45026.1; PID:G28336
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, alpha-actinin-1 and alpha-actinin-2.
 C:Genetics:
 A:Gene: GDB:ACTB
 A:Cross-references: GDB:118964; OMIM:102630
 A:Map position: 7p22-7p22
 A:Introns: 41/3; 121/3; 268/1; 328/3
 C:Superfamily: actin
 C:Keywords: Cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis; F-actin; F-actin monomer; actin beta #status predicted <MAT>
 F:2-375/Product: actin beta #status predicted <MAT>
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSTTTAE 15
 Db 191 KILTERGYSTTTAE 205

Search completed: April 8, 2005, 10:53:07
 Job time : 9.33333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-11
Perfect score: 75
Sequence: 1 KILTERGYSTTTAE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	33	Q6V107	Q6V107 mus spretus
2	75	100.0	39	Q6S3E7	Q6S3E7 poecilia re
3	75	100.0	93	Q6VQP9	Q6VQP9 romalea mic
4	75	100.0	101	Q61569	Q61569 osteragla
5	75	100.0	104	Q11210	Q11210 macaca fasc
6	75	100.0	109	Q28916	Q28916 macaca fusc
7	75	100.0	124	Q9FY43	Q9FY43 trebouxia j
8	75	100.0	125	Q802E1	Q802E1 zoarces viv
9	75	100.0	125	Q802E2	Q802E2 pachycara b
10	75	100.0	128	Q852Q7	Q852Q7 marchantia
11	75	100.0	130	Q865G0	Q865G0 capra hircu
12	75	100.0	132	Q91A84	Q91A84 stizostedio
13	75	100.0	133	Q9U4L7	Q9U4L7 ageniapiis
14	75	100.0	133	Q9U4L8	Q9U4L8 ageniapiis
15	75	100.0	133	Q9U4L9	Q9U4L9 ageniapiis
16	75	100.0	133	Q9U4M0	Q9U4M0 ageniapiis
17	75	100.0	136	Q95V64	Q95V64 ixodes scap
18	75	100.0	137	Q8H1A1	Q8H1A1 nicotiana b
19	75	100.0	140	Q68U00	Q68U00 lepeophthei
20	75	100.0	142	Q9BGH4	Q9BGH4 oryctolagus
21	75	100.0	145	Q91L42	Q91L42 trebouxia j
22	75	100.0	146	Q9Y191	Q9Y191 pleocoglossu
23	75	100.0	150	Q68AX1	Q68AX1 cynops pyrr
24	75	100.0	159	Q8MVL3	Q8MVL3 boltenia vi
25	75	100.0	160	Q8T6A7	Q8T6A7 trichinella
26	75	100.0	160	Q9NAS3	Q9NAS3 blattella g
27	75	100.0	164	Q8MVP9	Q8MVP9 boltenia vi
28	75	100.0	167	Q76D36	Q76D36 costus spec
29	75	100.0	167	Q76D37	Q76D37 costus spec
30	75	100.0	169	Q8SPK6	Q8SPK6 sus scrofa
31	75	100.0	171	Q766D6	Q766D6 phyllostach

32	75	100.0	171	2	Q7XAK3	Q7XAK3 asparagus o
33	75	100.0	171	2	Q8JH59	Q8JH59 chelydra se
34	75	100.0	171	2	Q6GXE6	Q6GXE6 lepisosteus
35	75	100.0	171	2	Q72W59	Q72W59 rana cateab
36	75	100.0	172	2	Q869B3	Q869B3 botryllus s
37	75	100.0	173	2	Q6RX10	Q6RX10 ficus caric
38	75	100.0	174	2	Q819W1	Q819W1 biomphalari
39	75	100.0	174	2	Q819W2	Q819W2 biomphalari
40	75	100.0	174	2	Q819W3	Q819W3 biomphalari
41	75	100.0	174	2	Q819W4	Q819W4 biomphalari
42	75	100.0	174	2	Q819W5	Q819W5 biomphalari
43	75	100.0	174	2	Q819W6	Q819W6 helisoma an
44	75	100.0	174	2	Q819W7	Q819W7 helisoma tr
45	75	100.0	174	2	Q819W8	Q819W8 biomphalari

ALIGNMENTS

RESULT 1
Q6V107 PRELIMINARY; PRT; 33 AA.
AC Q6V107; 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Beta-actin (Fragment).
CN Name=Actb;
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUES=Liver;
RA Cabrera-Luque J.M., Prieto-Alamo M.J., Pueyo C.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY355144; AAQ55830.1; -
FT NON_TER 1
FT NON_TER 33
SQ SEQUENCE 33 AA; 3892 MW; 48ACD0E5344AA20B CRC64;

Query Match 100.0%; Score 75; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSTTTAE 15
Db 3 KILTERGYSTTTAE 17

RESULT 2
Q6S3E7 PRELIMINARY; PRT; 39 AA.
ID Q6S3E7;
AC Q6S3E7; 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Beta-actin (Fragment).
OS Poecilia reticulata (Guppy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Poecilia.
OX NCBI_TaxID=8081;
RN [1]
RP SEQUENCE FROM N.A.
RA Hallgren S.L.E., Olsen H.K.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY478389; AAR99700.1; -
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4546 MW; 7BED3DB5437E4D49 CRC64;

Fri Apr 8 14:14:18 2005

us-09-423-351c-11.rup

Query Match 100.0%; Score 75; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
DB 15 KILTERGYSFTTAAE 29

RESULT 3

Q6VQP9 PRELIMINARY; PRT; 93 AA.
AC Q6VQP9; 27, Created
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DE Actin (Fragment).
OS Romalea microptera (nubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE FROM N.A.
RA Fei H., Martin T., Jaskowiack K., Hatle J., Borst D.W.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV331667; AAQ24502.1; --
FT NON_TER 1
SQ SEQUENCE 93 AA; 10698 MW; 5635F535A532256 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
DB 33 KILTERGYSFTTAAE 47

RESULT 4

O61569 PRELIMINARY; PRT; 101 AA.
AC O61569;
DT 01-AUG-1998 (TREMELrel. 07, Created)
DT 01-AUG-1998 (TREMELrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name-act;
OS Osteragia osteragi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
OX NCBI_TaxID=6317;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20233682; PubMed=10769181; DOI=10.1042/0264-6021:3470763;
RA Moore J., Tetley L., Devaney E.;
RT "Identification of abundant mRNAs from the third stage larvae of the parasitic nematode, Osteragia osteragi.";
RL Biochem. J. 347:763-770(2000).
DR EMBL; AF052043; AAC06292.1; --
FT HSP; P10983; 104X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
SQ SEQUENCE 101 AA; 11499 MW; 7AF3A21892AD0D75 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
DB 28 KILTERGYSFTTAAE 42

RESULT 5

Q11210 PRELIMINARY; PRT; 104 AA.
AC Q11210;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Hino A., Tokuyama Y., Kobayashi M., Yano M., Weir B., Takeda J.,
RA Bell G.I., Macdonald R.L.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20576; AAA62435.1; --
DR HSP; P10983; 104X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
SQ SEQUENCE 104 AA; 11438 MW; 3610F3FEFA370C91 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
DB 62 KILTERGYSFTTAAE 76

RESULT 6

Q28916 PRELIMINARY; PRT; 109 AA.
AC Q28916;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Actin (Fragment).
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071113; PubMed=757717; DOI=10.1016/0960-0760(95)00157-U;
RA Yamada-Mouri N., Hirata S., Hayaishi M., Kato J.;
RT "Analysis of the expression and the first exon of aromatase mRNA in monkey brain.";
RL J. Steroid Biochem. Mol. Biol. 55:17-23(1995).
DR EMBL; S79782; AAB35618.2; --
DR HSP; P10983; 104X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
SQ SEQUENCE 109 AA; 12333 MW; 64A64E108CDDA54C CRC64;

Query Match 100.0%; Score 75; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
DB 76 KILTERGYSFTTAAE 90
|||||

RESULT 7

ID Q9FY43 PRELIMINARY; PRT; 124 AA.
AC Q9FY43;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Actin type I (fragment).
OS Trebouxia jamesii 'vulpinae'.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxioophyceae;
OC Microthamniales; Trebouxia.
OX NCBI_TaxID=134429;
RN [1]
RP SEQUENCE FROM N.A.
RA Kroken S., Taylor J.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.

DR EMBL; AY005404; AAF97494.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
KW Structural protein.
FT NON_TER 1
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 13781 MW; 83AF18D241C8CD8E CRC64;

Query Match 100.0%; Score 75; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
DB 69 KILTERGYSFTTAAE 83
|||||

RESULT 8

ID Q802E1 PRELIMINARY; PRT; 125 AA.
AC Q802E1;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Beta actin (fragment).
GN Name=ACT-B;
OS Zoarces viviparus (Belpout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Zoarcoidei;
OC Zoarcidae; Zoarces.
OX NCBI_TaxID=48416;
RN [1]
RP SEQUENCE FROM N.A.
RA Lucassen M., Sokolov E., Poertner H.-O.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).

CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY227658; AAO72722.1; -.
DR HSSP; P60712; 1HLJ.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 14100 MW; 7B33EA4CF5EA88B0 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
DB 105 KILTERGYSFTTAAE 119
|||||

RESULT 9

ID Q802E2 PRELIMINARY; PRT; 125 AA.
AC Q802E2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Beta actin (fragment).
GN Name=ACT-B;
OS Pachycara brachycephalum (Antarctic eelpout) (Austrolycichthys
brachycephalus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Zoarcoidei;
OC Zoarcidae; Pachycara.
OX NCBI_TaxID=36221;
RN [1]
RP SEQUENCE FROM N.A.
RA Lucassen M., Sokolov E., Poertner H.-O.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).

CC -!- SIMILARITY: Belongs to the actin family.

DR EMBL; AY227657; AAO72721.1; -.
DR HSSP; P60712; 1HLJ.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 14100 MW; 7B33EA4CF5EA88B0 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAAE 15
DB 105 KILTERGYSFTTAAE 119
|||||

RESULT 10

Q852Q7 PRELIMINARY; PRT; 128 AA.
ID Q852Q7
AC Q852Q7;

```

Db 106 KILTERGYSFTTTAE 120
RESULT 12
Q9TA84 PRELIMINARY; PRT; 132 AA.
ID Q9IA84
AC Q9IA84;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta actin (Fragment).
OS Stizostedion vitreum.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Percidae; Stizostedion.
OC NCBI_TaxID=57868;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermal sarcoma;
RX MEDLINE=21109119; PubMed=11162816; DOI=10.1006/viro.2000.0731;
RA Rovnak J.; Casey J.W.; Quackenbush S.L.;
RT "Intracellular targeting of wallye dermal sarcoma virus Orf A (rv-
cyclo).".
RL Virology 280:31-40(2001).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC EMBL; AF219944; AAF31439.1; -.
DR HSP; P60712; IHLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 132
FT NON_TER 132
SQ SEQUENCE 132 AA; 14886 MW; D78E91F800A65E8E CRC64;

Query Match 100.0%; Score 75; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTTAE 15
DB 102 KILTERGYSFTTTAE 116

RESULT 13
Q9U4L7 PRELIMINARY; PRT; 133 AA.
ID Q9U4L7
AC Q9U4L7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Actin 2 (Fragment).
OS Acanthopterygii; Neopterygii; Teleostei; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Percidae; Stizostedion.
OC NCBI_TaxID=57868;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Taiwan population;
RX MEDLINE=21109119; PubMed=11162816; DOI=10.1006/viro.2000.0731;
RA Rovnak J.; Casey J.W.; Quackenbush S.L.;
RT "Intracellular targeting of wallye dermal sarcoma virus Orf A (rv-
cyclo).".
RL Virology 280:31-40(2001).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC EMBL; AF481159; AAO49278.1; -.
DR HSP; P60712; IHLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 130
FT NON_TER 130
SQ SEQUENCE 130 AA; 14728 MW; E817FD365B33EA3F CRC64;

Query Match 100.0%; Score 75; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTTAE 15
DB 102 KILTERGYSFTTTAE 116

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CC      in all eukaryotic cells (By similarity).
CC      -!- SIMILARITY: Belongs to the actin family.
DR      EMBL; AF164631; AAF22279.1; -.
DR      HSSP; P10983; 1D4X.
DR      GO; GO:0015629; C:actin cytoskeleton; IEA.
DR      GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR      InterPro; IPR004000; Actin_like.
DR      Pfam; PF00022; Actin; 1.
DR      PRINTS; PR00190; ACTIN.
DR      PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW      Structural protein.
FT      NON_TER 1
FT      NON_TER 133
SQ      SEQUENCE 133 AA; 14955 MW; 27DFC1FF30D4984F CRC64;

  Query Match      100.0%; Score 75; DB 2; Length 133;
  Best Local Similarity 100.0%; Pred. No. 4.9e-05;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KILTERGYSFTTTAE 15
Db      |||||
        103 KILTERGYSFTTTAE 117

RESULT 14
Q9U4L8      PRELIMINARY; PRT; 133 AA.
AC      Q9U4L8;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Actin 1 (Fragment).
OS      Agenesiaspis citricola.
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
OC      Encyrtidae; Encyrtinae; Agenesiaspis.
OX      NCBI_TaxID=105762;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Taiwan population;
RA      Hoy M.A., Jeyaprasath A., Morakote R., Lo P.K.C., Nguyen R.;
RT      "Genomic analyses of two populations of Agenesiaspis citricola
      (Hymenoptera: Encyrtidae) suggest that a cryptic species may exist.";
RL      Biol. Control 17:1-10(2000).
CC      -!- FUNCTION: Actins are highly conserved proteins that are involved
CC      in various types of cell motility and are ubiquitously expressed
CC      in all eukaryotic cells (By similarity).
CC      -!- SIMILARITY: Belongs to the actin family.
DR      EMBL; AF164630; AAF22278.1; -.
DR      HSSP; P10983; 1D4X.
DR      GO; GO:0015629; C:actin cytoskeleton; IEA.
DR      GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR      InterPro; IPR004000; Actin_like.
DR      Pfam; PF00022; Actin; 1.
DR      PRINTS; PR00190; ACTIN.
DR      PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW      Structural protein.
FT      NON_TER 1
FT      NON_TER 133
SQ      SEQUENCE 133 AA; 14941 MW; 62CB94EF37A39F3F CRC64;

  Query Match      100.0%; Score 75; DB 2; Length 133;
  Best Local Similarity 100.0%; Pred. No. 4.9e-05;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KILTERGYSFTTTAE 15
Db      |||||
        103 KILTERGYSFTTTAE 117

RESULT 15
Q9U4L9      PRELIMINARY; PRT; 133 AA.
ID      Q9U4L9
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AC      Q9U4L9;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Actin 2 (Fragment).
OS      Agenesiaspis citricola.
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
OC      Encyrtidae; Encyrtinae; Agenesiaspis.
OX      NCBI_TaxID=105762;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Australian population derived;
RA      Hoy M.A., Jeyaprasath A., Morakote R., Lo P.K.C., Nguyen R.;
RT      "Genomic analyses of two populations of Agenesiaspis citricola
      (Hymenoptera: Encyrtidae) suggest that a cryptic species may exist.";
RL      Biol. Control 17:1-10(2000).
CC      -!- FUNCTION: Actins are highly conserved proteins that are involved
CC      in various types of cell motility and are ubiquitously expressed
CC      in all eukaryotic cells (By similarity).
CC      -!- SIMILARITY: Belongs to the actin family.
DR      EMBL; AF164629; AAF22277.1; -.
DR      HSSP; P10983; 1D4X.
DR      GO; GO:0015629; C:actin cytoskeleton; IEA.
DR      GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR      InterPro; IPR004000; Actin_like.
DR      Pfam; PF00022; Actin; 1.
DR      PRINTS; PR00190; ACTIN.
DR      PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW      Structural protein.
FT      NON_TER 1
FT      NON_TER 133
SQ      SEQUENCE 133 AA; 14955 MW; 27DFC1FF30D4984F CRC64;

  Query Match      100.0%; Score 75; DB 2; Length 133;
  Best Local Similarity 100.0%; Pred. No. 4.9e-05;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KILTERGYSFTTTAE 15
Db      |||||
        103 KILTERGYSFTTTAE 117

Search completed: April 8, 2005, 12:03:13
Job time : 57.8667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-12

Perfect score: 75

Sequence: 1 RGYSTTTVAEREIVR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	75	100.0	15	2 AAW92538	Beta-acti
2	75	100.0	97	4 AAM13687	Aam13687 Peptide #
3	75	100.0	97	4 ABB32618	Abb32618 Peptide #
4	75	100.0	97	4 AAM26087	Aam26087 Peptide #
5	75	100.0	97	4 ABB27467	Abb27467 Human pep
6	75	100.0	97	4 ABB18116	Abb18116 Protein #
7	75	100.0	97	4 AAM65825	Human bon
8	75	100.0	97	4 AAM53448	Aam53448 Human bra
9	75	100.0	97	4 ABB47471	Human liv
10	75	100.0	97	4 AAM01437	Aam01437 Peptide #
11	75	100.0	97	5 ABB35459	Abb35459 Human pep
12	75	100.0	153	4 ABB15497	Abb15497 Novel hum
13	75	100.0	164	3 AAG37312	Aag37312 Arabidops
14	75	100.0	168	5 ABB42912	Abb42912 Human ova
15	75	100.0	186	3 AAG38701	Aag38701 Arabidops
16	75	100.0	186	3 AAG47774	Aag47774 Arabidops
17	75	100.0	196	6 ABB70816	Abb70816 Human adi
18	75	100.0	229	3 AAG38700	Aag38700 Arabidops
19	75	100.0	246	3 AAG38699	Aag38699 Arabidops
20	75	100.0	274	6 ABB70549	Abb70549 Human adi
21	75	100.0	276	3 AAG50947	Aag50947 Arabidops
22	75	100.0	277	3 AAG05115	Aag05115 Arabidops
23	75	100.0	294	7 ABB163068	Abb163068 Human apo
24	75	100.0	304	3 AAG50946	Aag50946 Arabidops
25	75	100.0	305	3 AAG05114	Aag05114 Arabidops

26	75	100.0	321	3 AAG50945	Aag50945 Arabidops
27	75	100.0	322	3 AAG05113	Aag05113 Arabidops
28	75	100.0	332	3 AAG50873	Aag50873 Arabidops
29	75	100.0	332	3 AAG37317	Aag37317 Arabidops
30	75	100.0	332	3 AAG44697	Aag44697 Zea mays
31	75	100.0	332	3 AAG24178	Aag24178 Arabidops
32	75	100.0	332	3 AAG05583	Aag05583 Arabidops
33	75	100.0	332	3 AAG47761	Aag47761 Arabidops
34	75	100.0	332	3 AAG50944	Aag50944 Arabidops
35	75	100.0	332	3 AAG34599	Aag34599 Arabidops
36	75	100.0	332	3 AAG54243	Aag54243 Arabidops
37	75	100.0	332	3 AAG47770	Aag47770 Arabidops
38	75	100.0	332	7 ADI63011	ADI63011 Human apo
39	75	100.0	345	3 AAG47748	Aag47748 Arabidops
40	75	100.0	360	3 AAG47760	Aag47760 Arabidops
41	75	100.0	360	3 AAG47769	Aag47769 Arabidops
42	75	100.0	360	3 AAG50872	Aag50872 Arabidops
43	75	100.0	360	3 AAG05582	Aag05582 Arabidops
44	75	100.0	360	3 AAG34598	Aag34598 Arabidops
45	75	100.0	360	3 AAG37316	Aag37316 Arabidops

ALIGNMENTS

RESULT 1

AAW92538
ID AAW92538 standard; peptide; 15 AA.

XX AC AAW92538;

XX DT 26-APR-1999 (first entry)

XX DE Beta-actin reference peptide substrate #12.

XX KW Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity.

XX OS Synthetic.

XX PN WO9853322-A1.

XX PD 26-NOV-1998.

XX PF 22-MAY-1998; 98WO-GB001485.

XX PR 23-MAY-1997; 97GB-00010762.

XX PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

XX PI Willison K, Hynes G, Liou AK;

XX WPI; 1999-070162/06.

PT Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

XX Disclosure; Fig 10; 97pp; English.

CC This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

CC agents may target cells that are actively synthesising tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AAW92527-W92541 are
 CC peptide substrates used in the method of the invention
 XX
 XX Sequence 15 AA;

Query Match 100.0%; Score 75; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
 |||||
 DB 1 RGYSTTTAEREIVR 15

RESULT 2
 AAM13687
 ID AAM13687 standard; protein; 97 AA.
 AC AAM13687;
 XX
 XX 12-OCT-2001 (first entry)

DE Peptide #121 encoded by probe for measuring cervical gene expression.
 XX Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX Homo sapiens.
 OS
 XX WO200157278-A2.
 PN
 XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000670.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488901/53.
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 18513; 487bp; English.
 XX The present invention relates to human single exon nucleic acid probes
 CC (SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
 |||||
 DB 75 RGYSTTTAEREIVR 89

RESULT 3
 ABB32618
 ID ABB32618 standard; peptide; 97 AA.
 XX
 AC ABB32618;
 XX
 XX 04-FEB-2002 (first entry)

XX Peptide #124 encoded by human foetal liver single exon probe.
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX Homo sapiens.
 OS
 XX WO200157277-A2.
 PN
 XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483447/52.
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 25253; 639pp + Sequence Listing; English.
 XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
 |||||
 DB 75 RGYSTTTAEREIVR 89

RESULT 4
 AAM26087
 ID AAM26087 standard; protein; 97 AA.
 XX
 AC AAM26087;
 XX
 XX 17-OCT-2001 (first entry)

XX Peptide #124 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 26356; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP;
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders

SQ Sequence 97 AA;
Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGYSTTTTAEREIVR 15

DB 75 RGYSTTTTAEREIVR 89

RESULT 5

ABB27467

ID ABB27467 standard; peptide; 97 AA.

XX ABB27467;

XX 01-FEB-2002 (first entry)

XX Human peptide #118 encoded by breast cell single exon nucleic acid probe.
DE Human; microarray; single exon probe; gene expression; breast; disease;
XX cancer.

XX Homo sapiens.

XX WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000662.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.

XX Claim 27; SEQ ID NO 10435; 327pp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode protein. They
CC are useful for gene discovery, and for determining predisposition and/or
CC assessing breast disease. Gene expression analysis is useful for
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGYSTTTTAEREIVR 15

DB 75 RGYSTTTTAEREIVR 89

RESULT 6

ABB18116

ID ABB18116 standard; protein; 97 AA.

XX ABB18116;

XX 23-JAN-2002 (first entry)

XX Protein #115 encoded by probe for measuring heart cell gene expression.
DE Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

Fri Apr 8 14:14:18 2005

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 26131; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
XX Sequence 97 AA;
SQ
Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.6e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGYSTTTTAREIVR 15
Db 75 RGYSTTTTAREIVR 89
RESULT 8
AAM53448
ID AAM53448 standard; protein; 97 AA.
XX
XX AAM53448;
XX
XX 05-NOV-2001 (first entry)
DT Human brain expressed single exon probe encoded protein SEQ ID NO: 25553.
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
KW Homo sapiens.
XX WO200157275-A2.
XX
XX 09-AUG-2001.
PD
PF 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
PT
XX Example 4; SEQ ID NO 25553; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX Sequence 97 AA;
SQ

PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488999/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
PT
XX Claim 15; SEQ ID NO 19886; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease.
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 97 AA;
SQ
Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.6e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGYSTTTTAREIVR 15
Db 75 RGYSTTTTAREIVR 89
RESULT 7
AAM65825
ID AAM65825 standard; protein; 97 AA.
XX
XX AAM65825;
XX
XX 06-NOV-2001 (first entry)
DT Human bone marrow expressed probe encoded protein SEQ ID NO: 26131.
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.
KW Homo sapiens.
XX WO200157276-A2.
XX
XX 09-AUG-2001.
PD
PF 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488900/53.
XX
XX

Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
|||||
DB 75 RGYSTTTAEREIVR 89

RESULT 9
ABG47471
ID ABG47471 standard; peptide; 97 AA.

XX AC ABG47471;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID NO 26119.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.

XX PN WO200157273-A2.
XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PS WPI; 2001-488898/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human adult liver.

XX PS Claim 27; SEQ ID NO 26119; 658pp; English.

XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (I) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABG47348-ABG59930 represent human
XX CC liver single exon encoded peptides of the invention. Note: The sequence
XX CC information for this patent does not appear in the printed specification
XX CC but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
|||||

Db 75 RGYSTTTAEREIVR 89
RESULT 10
AAM01437
ID AAM01437 standard; protein; 97 AA.
XX AC AAM01437;
XX DT 09-OCT-2001 (first entry)

XX DE Peptide #119 encoded by probe for measuring human breast gene expression.
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.

XX PN WO200157270-A2.

XX PD 09-AUG-2001.

XX PF 29-JAN-2001; 2001WO-US000661.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PS WPI; 2001-476286/51.

XX PT Novel single exon nucleic acid probe used to measuring gene expression in
XX PT a human breast.
XX PS Claim 27; SEQ ID NO 10177; 322pp; English.
XX CC The present invention relates to novel single exon nucleic acid probes
XX CC (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for measuring human gene expression in
XX CC a human breast sample, where the probe hybridises at high stringency to a
XX CC nucleic acid expressed in the human breast. The probes are useful for
XX CC predicting, diagnosing, grading, staging, monitoring and prognosing
XX CC diseases of the human breast, particularly those diseases with polygenic
XX CC aetiology. The diseases include: breast cancer; disorders of polycystic
XX CC inflammatory diseases of the breast; fibrocystic changes; proliferative
XX CC breast disease and non-carcinoma tumours. Note: The sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
|||||
DB 75 RGYSTTTAEREIVR 89

RESULT 11
ABG35459
ID ABG35459 standard; peptide; 97 AA.
XX AC ABG35459;

CC histiocytosis, lymphangioliomyomatosis, pulmonary alveolar proteinosis,
 CC Kargener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 97 AA;
 Query Match 100.0%; Score 75; DB 5; Length 97;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGYSTTTTAREIVR 15
 DB 75 RGYSTTTTAREIVR 89
 RESULT 12
 ABG15497
 ID ABG15497 standard; protein; 153 AA.
 XX
 AC ABG15497;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #15488.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 FN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI
 XX
 XX WPI: 2001-639362/73.
 DR N-PSDB; AAS79684.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 45856; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and

XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 25124.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioliomyomatosis; Kargener syndrome;
 KW primary ciliary dyskinesia; fibrocystic pulmonary dysplasia;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 FN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GH-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX
 XX WPI: 2002-114183/15.
 DR
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 PS Claim 27; SEQ ID NO 25124; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 153 AA;

Query Match 100.0%; Score 75; DB 4; Length 153;
 Best Local Similarity 100.0%; Pred. No. 9.1e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

QY 1 RGYSTTTAERIVR 15
 |||||
 Db 37 RGYSTTTAERIVR 51

RESULT 13
 AAG37312
 ID AAG37312 standard; protein; 164 AA.

XX AAG37312;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 45859.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0121180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 19-APR-1999; 99US-0129845P.

PR 21-APR-1999; 99US-0130077P.

PR 23-APR-1999; 99US-0130499P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 07-MAY-1999; 99US-0132487P.

PR 11-MAY-1999; 99US-0132487P.

PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
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XX	DE	Human ovarian antigen HPDQZ65, SEQ ID NO:4044.					
XX	KW	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;					
KW	KW	ovarian cancer; breast cancer; tumour; reproductive system disorder;					
KW	KW	infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;					
KW	KW	PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;					
KW	KW	inflammatory condition; immune disorder; blood disorder;					
KW	KW	cardiovascular disorder; respiratory system disorder; neurological disorder;					
KW	KW	gastrointestinal disorder; urinary system disorder; drug screening;					
KW	KW	gene therapy; chromosome mapping; immunomodulatory; neuroprotective;					
KW	KW	antibody preparation; cytostatic; immunomodulatory; reproductive;					
XX	OS	antiinflammatory; gynaecological; reproductive.					
XX	OS	Homo sapiens.					
XX	PN	WO200200677-A1.					
XX	PD	03-JAN-2002.					
XX	PF	07-JUN-2001; 2001WO-US018569.					
XX	XX	07-JUN-2000; 2000US-0209467P.					
XX	XX	(HUMA-) HUMAN GENOME SCI INC.					
XX	PI	Birse CE, Rosen CA;					
XX	DR	WPI; 2002-147878/19.					
XX	DR	N-PSDB; ABQ55989.					
XX	PT	Isolated nucleic acid molecules encoding novel ovarian polypeptides,					
PT	PT	useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian					
PT	PT	cancer), immune disorders, cardiovascular disorders and neurological					
PT	PT	diseases.					
XX	PS	Claim 11; SEQ ID NO 4044; 2922pp; English.					
XX	CC	The invention relates to 2175 novel human ovarian antigens (ABP41054-					
CC	CC	ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also					
CC	CC	encompasses polypeptides 90% identical and polynucleotides 95% identical					
CC	CC	to the sequences of the invention. The invention additionally relates to					
CC	CC	recombinant vectors and host cells comprising human ovarian antigen					
CC	CC	polynucleotides, antibodies against human ovarian antigens, and the use					
CC	CC	of ovarian antigen polynucleotides and polypeptides in diagnosing,					
CC	CC	treating, prognosing or preventing various ovarian cancer and breast cancer,					
CC	CC	disorders. Such conditions include ovarian cancer and breast cancer, and					
CC	CC	metastatic tumours of ovarian or breast origin, reproductive system					
CC	CC	disorders (e.g., infertility, disorders of pregnancy, anovulation,					
CC	CC	polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine					
CC	CC	disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic					
CC	CC	shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and					
CC	CC	vaginitis), immune disorders (e.g., congenital and acquired					
CC	CC	immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),					
CC	CC	blood-related disorders (e.g., anaemia), cardiovascular disorders,					
CC	CC	respiratory disorders, neurological disorders, gastrointestinal disorders					

CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 168 AA;

Query Match 100.0%; Score 75; DB 5; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
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 Db 82 RCYSFTTTAERIVR 96

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AC AAG38701;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 47783.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

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XX 25-FEB-2000; 2000EP-00301439.

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XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

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Job time : 62.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-12

Perfect score: 75

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	75	100.0	375	4	US-09-976-594-731
5	75	100.0	399	4	US-09-949-016-6656
6	75	100.0	404	4	US-09-949-016-11313
7	71	94.7	377	4	US-09-248-796A-14109
8	70	93.3	239	4	US-09-949-016-10409
9	70	93.3	375	2	US-08-494-151-14
10	70	93.3	375	3	US-09-106-217-16
11	70	93.3	376	1	US-08-588-113-2
12	70	93.3	376	4	US-09-949-016-6100
13	70	93.3	377	3	US-09-106-217-2
14	70	93.3	377	4	US-09-919-172-33
15	70	93.3	377	4	US-09-917-254-53
16	70	93.3	386	4	US-09-949-016-7721
17	70	93.3	402	4	US-09-949-016-10757
18	68	90.7	375	3	US-09-171-337A-7
19	68	90.7	375	3	US-09-171-337A-8
20	68	90.7	375	4	US-09-631-022-7
21	68	90.7	375	4	US-09-631-022-8
22	65	86.7	371	1	US-08-261-206A-77
23	52	69.3	10	4	US-09-786-066-11
24	40	53.3	394	4	US-09-949-016-6655
25	40	53.3	406	4	US-09-949-016-7396
26	40	53.3	494	4	US-09-270-767-42129
27	39	52.0	169	4	US-09-902-540-14165

28	39	52.0	277	4	US-09-248-796A-17761	Sequence 17761, A
29	39	52.0	400	4	US-09-792-024-99	Sequence 99, Appl
30	38	50.7	279	4	US-09-270-767-41981	Sequence 41981, A
31	38	50.7	376	4	US-09-538-092-1110	Sequence 1110, Ap
32	38	50.7	376	4	US-09-949-016-6656	Sequence 6656, Ap
33	38	50.7	376	4	US-09-949-016-8452	Sequence 8452, Ap
34	38	50.7	384	4	US-09-538-092-395	Sequence 395, App
35	38	50.7	433	4	US-09-614-912-168	Sequence 168, App
36	38	50.7	631	3	US-09-147-119-7	Sequence 7, Appli
37	38	50.7	651	4	US-09-489-039A-10691	Sequence 10691, A
38	38	50.7	707	4	US-09-949-016-8495	Sequence 8495, Ap
39	37	49.3	103	4	US-09-205-258-294	Sequence 294, App
40	37	49.3	250	4	US-09-270-767-40335	Sequence 40335, A
41	37	49.3	250	4	US-09-270-767-55551	Sequence 55551, A
42	37	49.3	362	4	US-09-949-016-7725	Sequence 7725, Ap
43	37	49.3	376	4	US-09-538-092-1109	Sequence 1109, Ap
44	37	49.3	423	4	US-09-252-991A-30653	Sequence 30653, A
45	37	49.3	609	3	US-09-115-475-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-306-446C-5
; Sequence 5, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyou Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P063440S0/BAS
; CURRENT APPLICATION NUMBER: US/09/306,446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-5

Query Match 100.0%; Score 75; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTAEREIVR 15
DB 75 RGYSTTTAEREIVR 89

RESULT 2

US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh
 SOFTWARE: Microsoft Word for Macintosh
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,236
 FILING DATE: March 1, 1996
 CLASSIFICATION: 514
 PRIOR APPLICATION NUMBER: 60/002,288
 FILING DATE: August 14, 1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Benjamin Aaron Adler, Ph.D.
 REGISTRATION NUMBER: 35,423
 REFERENCE/DOCKET NUMBER: D5807
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713-777-2321
 TELEFAX: 713-777-6908
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374
 TYPE: Amino acid
 STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE:
 DESCRIPTION: Protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 TISSUE TYPE:
 CELL TYPE:
 CELL LINE:

Query Match 100.0%; Score 75; DB 3; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAEREIVR 15
 Db 195 RGYSFTTTAEREIVR 209

RESULT 3
 US-09-306-446C-2
 ; Sequence 2, Application US/09306446C
 ; Patent No. 6372959
 ; GENERAL INFORMATION:
 ; APPLICANT: KIM, Dong Soo
 ; APPLICANT: KIM, Chul Geun
 ; APPLICANT: NAM, Yoon Kwon
 ; APPLICANT: NOH, Jae Koo
 ; APPLICANT: CHO, Kyou Nam
 ; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
 ; FILE REFERENCE: P06344U0/BAS
 ; CURRENT APPLICATION NUMBER: US/09/306,446C
 ; CURRENT FILING DATE: 1999-05-06
 ; PRIOR APPLICATION NUMBER: KR 98/20255
 ; PRIOR FILING DATE: 1998-06-01
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; TYPE: PRT
 ; ORGANISM: Misgurnus mizolepis
 ; US-09-306-446C-2

Query Match 100.0%; Score 75; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAEREIVR 15
 Db 196 RGYSFTTTAEREIVR 210

RESULT 4
 US-09-976-594-731
 ; Sequence 731, Application US/09976594
 ; Patent No. 6673549
 ; GENERAL INFORMATION:
 ; APPLICANT: Furness, Michael
 ; APPLICANT: Buchbinder, Jenny
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 ; FILE REFERENCE: PA-0041 US
 ; CURRENT APPLICATION NUMBER: US/09/976,594
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,409
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 1143
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 731
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
 ; US-09-976-594-731

Query Match 100.0%; Score 75; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAEREIVR 15
 Db 196 RGYSFTTTAEREIVR 210

RESULT 5
 US-09-949-016-9424
 ; Sequence 9424, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9424
 ; LENGTH: 399
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-9424

Query Match 100.0%; Score 75; DB 4; Length 399;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGYSFTTTAEREIVR 15
 Db 220 RGYSFTTTAEREIVR 234

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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10409
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10409

Query Match          93.3%; Score 70; DB 4; Length 239;
Best Local Similarity 93.3%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RGYSTTTTAEREIVR 15
DB      60 RGYSTTTTAEREIVR 74

RESULT 9
US-08-494-151-14
; Sequence 14, Application US/08494151
; Patent No. 5840528
; GENERAL INFORMATION:
; APPLICANT: Van Ooyen, Albert Johannes Joseph
; TITLE OF INVENTION: Transformation of Phaffia rhodozyma
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,151
; FILING DATE: 23-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20039.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-151-14

Query Match          93.3%; Score 70; DB 2; Length 375;
Best Local Similarity 93.3%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RGYSTTTTAEREIVR 15
DB      196 RGYPTTTTAEREIVR 210

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match          100.0%; Score 75; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGYSTTTTAEREIVR 15
DB      225 RGYSTTTTAEREIVR 239

RESULT 7
US-09-248-796A-14109
; Sequence 14109, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14109
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14109

Query Match          94.7%; Score 71; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00016;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGYSTTTTAEREIVR 15
DB      198 RGYSTTTTAEREIVR 212

RESULT 8
US-09-949-016-10409
; Sequence 10409, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-217-2

Query Match 93.3%; Score 70; DB 3; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGYSFVTTAEREIVR 15
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DB 198 RGYSFVTTAEREIVR 212

RESULT 14
US-09-919-172-33
Sequence 33, Application US/09919172
Patent No. 6673545
GENERAL INFORMATION:
APPLICANT: Paris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 377
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match 93.3%; Score 70; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGYSFVTTAEREIVR 15
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DB 198 RGYSFVTTAEREIVR 212

RESULT 15
US-09-917-254-53
Sequence 53, Application US/09917254
Patent No. 6703204
GENERAL INFORMATION:
APPLICANT: Mutter, George
APPLICANT: Baak, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/7224 (JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 53
LENGTH: 377
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 93.3%; Score 70; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGYSFVTTAEREIVR 15
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DB 198 RGYSFVTTAEREIVR 212

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OM protein - protein search, using sw model

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Title: US-09-423-351C-12

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Post-processing: Minimum Match 0%
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Database : Published Applications AA:*

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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	75	100.0	180	US-10-437-963-169247	Sequence 169247, A
5	75	100.0	230	US-10-767-701-42770	Sequence 42770, A
6	75	100.0	236	US-10-424-599-206389	Sequence 206389, A
7	75	100.0	237	US-10-424-599-143226	Sequence 143226, A
8	75	100.0	238	US-10-437-963-162706	Sequence 162706, A
9	75	100.0	249	US-10-767-701-43575	Sequence 43575, A
10	75	100.0	261	US-10-424-599-177530	Sequence 177530, A
11	75	100.0	288	US-10-425-114-57500	Sequence 57500, A
12	75	100.0	331	US-10-425-114-59172	Sequence 59172, A
13	75	100.0	371	US-10-322-281-68	Sequence 68, Appl

14	75	100.0	375	14	US-10-205-194-93	Sequence 93, Appl
15	75	100.0	375	14	US-10-316-253-88	Sequence 88, Appl
16	75	100.0	375	15	US-10-205-331-94	Sequence 94, Appl
17	75	100.0	375	15	US-10-260-708-82	Sequence 82, Appl
18	75	100.0	376	16	US-10-437-963-202420	Sequence 202420, A
19	75	100.0	377	15	US-10-424-599-222816	Sequence 222816, A
20	75	100.0	377	15	US-10-424-599-223492	Sequence 223492, A
21	75	100.0	377	15	US-10-425-114-661124	Sequence 661124, A
22	75	100.0	378	15	US-10-425-114-52458	Sequence 52458, A
23	75	100.0	378	15	US-10-425-114-59265	Sequence 59265, A
24	75	100.0	378	15	US-10-425-114-59967	Sequence 59967, A
25	75	100.0	378	15	US-10-425-114-61003	Sequence 61003, A
26	75	100.0	380	16	US-10-437-963-106736	Sequence 106736, A
27	75	100.0	380	16	US-10-437-963-187415	Sequence 187415, A
28	75	100.0	383	16	US-10-767-701-47319	Sequence 47319, A
29	75	100.0	391	16	US-10-437-963-130713	Sequence 130713, A
30	75	100.0	398	16	US-10-322-281-63	Sequence 63, Appl
31	75	100.0	413	9	US-09-925-301-1436	Sequence 1436, Ap
32	75	100.0	421	16	US-10-437-963-186750	Sequence 186750, A
33	72	96.0	375	15	US-10-369-493-5927	Sequence 5927, Ap
34	71	94.7	184	15	US-10-425-114-48706	Sequence 48706, A
35	71	94.7	254	15	US-10-425-114-69353	Sequence 69353, A
36	71	94.7	299	15	US-10-424-599-278431	Sequence 278431, A
37	71	94.7	375	15	US-10-369-493-1786	Sequence 1786, Ap
38	71	94.7	375	16	US-10-477-369-1	Sequence 1, Appli
39	71	94.7	377	15	US-10-424-599-162009	Sequence 162009, A
40	71	94.7	377	16	US-10-437-963-121952	Sequence 121952, A
41	71	94.7	377	16	US-10-437-963-148877	Sequence 148877, A
42	71	94.7	377	16	US-10-437-963-198295	Sequence 198295, A
43	71	94.7	377	16	US-10-767-701-47239	Sequence 47239, A
44	71	94.7	379	15	US-10-424-599-278432	Sequence 278432, A
45	71	94.7	381	15	US-10-424-599-280814	Sequence 280814, A

ALIGNMENTS

RESULT 1
US-09-864-761-33414
; Sequence 33414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

us-09-423-351c-12.rapb

Fri Apr 8 14:14:18 2005

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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33414
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 48
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 81
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 28
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 85
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 37
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 45
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 40
; OTHER INFORMATION: EST HUMAN HIT: BE217130.1, EVALUATE 3.00e-50
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUATE 4.00e-51
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUATE 4.00e-50
; US-09-864-761-33414

Query Match 100.0%; Score 75; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSFTTTAEREIVR 15
DB 75 RGYSFTTTAEREIVR 89

RESULT 2
US-10-264-049-4044
; Sequence 4044, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Bize et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133p1
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4044
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-4044

Query Match 100.0%; Score 75; DB 15; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSFTTTAEREIVR 15

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33414
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 48
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 81
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 28
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 85
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 37
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 45
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 40
; OTHER INFORMATION: EST HUMAN HIT: BE217130.1, EVALUATE 3.00e-50
; OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUATE 4.00e-51
; OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUATE 4.00e-50
; US-09-864-761-33414

Query Match 100.0%; Score 75; DB 16; Length 179;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSFTTTAEREIVR 15
DB 74 RGYSFTTTAEREIVR 88

RESULT 4
US-10-437-963-169247
; Sequence 169247, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169247
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67685C.1.pep
US-10-437-963-169247

Query Match 100.0%; Score 75; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSFTTTAEREIVR 15
DB 74 RGYSFTTTAEREIVR 88

RESULT 4
US-10-437-963-169247
; Sequence 169247, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169247
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67685C.1.pep
US-10-437-963-169247

Query Match 100.0%; Score 75; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSFTTTAEREIVR 15
DB 74 RGYSFTTTAEREIVR 88

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; Sequence 143226, Application US/10424599

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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57500
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROB73004G09_FLI.pep
US-10-425-114-57500

Query Match 100.0%; Score 75; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 RGYSTTTTAAEREIVR 15
Db 109 RGYSTTTTAAEREIVR 123

RESULT 12
US-10-425-114-59172
; Sequence 59172, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59172
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700332871_FLI.pep
US-10-425-114-59172

Query Match 100.0%; Score 75; DB 15; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00011; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 RGYSTTTTAAEREIVR 15
Db 152 RGYSTTTTAAEREIVR 166

RESULT 13
US-10-322-281-68
; Sequence 68, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371

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TYPE: PRT
ORGANISM: Homo sapiens
US-10-322-281-68

Query Match 100.0%; Score 75; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAEREIVR 15
DB 196 RGYSTTTTAEREIVR 210

RESULT 14

US-10-205-194-93
; Sequence 93, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; OTHER INFORMATION: Cytoplasmic gamma isoform of actin
US-10-205-194-93

Query Match 100.0%; Score 75; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGYSTTTTAEREIVR 15
DB 196 RGYSTTTTAEREIVR 210

RESULT 15

US-10-316-253-88
; Sequence 88, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 886SM
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-88

Query Match 100.0%; Score 75; DB 14; Length 375;

Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGYSTTTTAEREIVR 15
DB 196 RGYSTTTTAEREIVR 210

Search completed: April 8, 2005, 12:51:01
Job time : 42.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-10

Perfect score: 71

Sequence: 1 IQAVLSLYASGRRTTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	155	A60945	actin homolog FAT,
2	71	100.0	195	S20097	actin 85c - potato
3	71	100.0	205	T07423	actin - Chlorella
4	71	100.0	308	A03000	actin 3 - fruit fl
5	71	100.0	325	JC2008	actin homolog prot
6	71	100.0	327	S11452	actin (clone 302)
7	71	100.0	328	S05430	actin beta - grass
8	71	100.0	331	S24409	actin - brown alga
9	71	100.0	332	T46655	actin-related prot
10	71	100.0	349	B25819	actin, fetal skele
11	71	100.0	361	S68089	actin 2 - Arabidop
12	71	100.0	362	A26559	actin type 5, cyto
13	71	100.0	362	S68090	actin 8 - Arabidop
14	71	100.0	365	S49007	actin - Pythium ir
15	71	100.0	365	A37431	actin, type 1 - Em
16	71	100.0	374	ATBOB	actin beta - bovin
17	71	100.0	374	ATBOG	actin gamma - bovi
18	71	100.0	374	JC5818	gamma-actin - huma
19	71	100.0	375	ATBOSM	actin, aortic smoo
20	71	100.0	375	ATRB	actin, skeletal mu
21	71	100.0	375	ATRTC	actin beta - rat
22	71	100.0	375	A48324	actin beta, cytosk
23	71	100.0	375	ATAX	actin - Acanthamo
24	71	100.0	375	ATACH	actin beta - chick
25	71	100.0	375	ATDO	actin - slime mold
26	71	100.0	375	ATHUB	actin beta - human
27	71	100.0	375	ATHUG	actin gamma 1 - hu
28	71	100.0	375	ATMSB	actin beta - mouse
29	71	100.0	375	ATMSG	actin gamma - mous

ALIGNMENTS

RESULT 1

A60945

actin homolog FAT, testicular - starfish (Pisaster ochraceus) (fragments)

C:Species: Pisaster ochraceus

C:Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C:Accession: A60945

R/Boom, J.D.G.; Smith, M.J.

J. Exp. Zool. 250, 312-320, 1989

A:Title: Molecular analyses of gene expression during sea star spermatogenesis.

A:Reference number: A60945; MUID:89341660; PMID:2474626

A:Accession: A60945

A:Molecule type: mRNA

A:Residues: 1-155 <BOO>

A:Cross-references: UNIPROT:Q7M3Y6

A:Note: authors translated the codon TTG for residue 77 as Ile, and TGC for residue 81

C:Superfamily: actin

Query Match 100.0%; Score 71; DB 2; Length 155;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15

Db 29 IQAVLSLYASGRRTTG 43

RESULT 2

S20097

actin 85c - potato (fragment)

C:Species: Solanum tuberosum (potato)

C:Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004

C:Accession: S20097

R/Drouin, G.; Dover, G.A.

J. Mol. Evol. 31, 132-150, 1990

A:Title: Independent gene evolution in the potato actin gene family demonstrated by phyl

A:Reference number: S20092; MUID:91012599; PMID:2120451

A:Accession: S20097

A:Molecule type: DNA

A:Residues: 1-195 <DRO>

A:Cross-references: UNIPROT:P30170; EMBL:X55747; NID:g21541; PIDN:CAA39277.1; PID:g13455

C:Genetics:

A:Introns: 132/1

C:Superfamily: actin

C:Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 71; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 2.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15

Db 118 IQAVLSLYASGRRTTG 132

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A:Accession: JC2008
A:Molecule type: mRNA
A:Residues: 1-325 <KAN>
A:Cross-references: GB:DI4612; NID:9434784; PIDN:BAA03463.1; PID:9434785
A:Experimental source: muscle
A:Superfamily: actin
C:Keywords: muscle contraction

Query Match 100.0%; Score 71; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
   |||||
DB 86 IQAVLSLYASGRRTTG 100

RESULT 6
S11452
actin (clone 302) - brine shrimp (fragment)
C:Species: Artemia sp. (brine shrimp)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S11452
R:Macias, M.T.; Sastre, L.
Nucleic Acids Res. 18, 5219-5225, 1990
A:Title: Molecular cloning and expression of four actin isoforms during Artemia
A:Reference number: S11450; MUID:90384823; PMID:2402445
A:Accession: S11452
A:Molecule type: mRNA
A:Residues: 1-327 <NAC>
A:Cross-references: UNIPROT:P18602; EMBL:X52604; NID:g5666; PIDN:CAA36837.1; PI
C:Superfamily: actin
C:Keywords: methylated amino acid; structural protein
F:25/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 71; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
   |||||
DB 88 IQAVLSLYASGRRTTG 102

RESULT 7
S05430
actin beta - grass carp
C:Species: Ctenopharyngodon idella (grass carp)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S05430
R:Liu, Z.; Zhu, Z.; Roberg, K.; Paras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Ha
Nucleic Acids Res. 17, 5850, 1989
A:Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A:Reference number: S05430; MUID:89345185; PMID:2762162
A:Accession: S05430
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-328 <LIU>
A:Cross-references: UNIPROT:P83751; EMBL:M25013
C:Genetics:
A:Introns: 41/3; 121/3; 268/1
C:Superfamily: actin
C:Keywords: cytoskeleton; methylated amino acid
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 71; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
   |||||
DB 136 IQAVLSLYASGRRTTG 150

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A;Cross-references: UNIPROT:Q61275; GB:X03767; GB:J00381; GB:M10652; NID:g49869; PTDN:C
C;Superfamily: actin
C;Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F;47/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 71; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
DB 110 IQAVLSLYASGRRTG 124
|||||
|||||

RESULT 11
S68089
actin 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 03-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68089
R;McDowell, J.M.; Huang, S.; McKinney, E.C.; An, Y.Q.; Meagher, R.B.
Genetics 142, 587-602, 1996
A;Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
A;Reference number: S68089; MUID:96158109; PMID:8852856
A;Accession: S68089
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-361 <MCD>
A;Cross-references: UNIPROT:Q93ZL9
A;Note: mRNA sequencing was also done
C;Genetics:
A;Gene: ACT2
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 71; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
DB 131 IQAVLSLYASGRRTG 145
|||||
|||||

RESULT 12
A26559
actin type 5, cytosolic - chicken
C;Species: Gallus gallus (Chicken)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C;Accession: A26559
R;Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A;Reference number: A26559; MUID:85213487; PMID:4000121
A;Accession: A26559
A;Molecule type: DNA
A;Residues: 1-362 <BER>
C;Superfamily: actin
C;Keywords: cytosol; methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 71; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
DB 137 IQAVLSLYASGRRTG 151
|||||
|||||

RESULT 13
S68090
actin 8 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68090
R;McDowell, J.M.; Huang, S.; McKinney, E.C.; An, Y.O.; Meagher, R.B.
Genetics 142, 587-602, 1996
A;Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
A;Reference number: S68089; MUID:96158109; PMID:8852856
A;Accession: S68090
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-362 <MCD>
A;Cross-references: UNIPROT:Q8LB94
A;Note: mRNA sequencing was also done
C;Genetics:
A;Gene: ACT8
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 71; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15
| | | | | | | | | | | | | | | | | |
Db 132 IQAVLSLYASGRRTTG 146

RESULT 14
S49007
actin - Pythium irregulare (fragment)
C;Species: Pythium irregulare
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
C;Accession: S49007
R;Bhattacharya, D.; Stickel, S.K.
J. Mol. Evol. 39, 56-61, 1994
A;Title: Sequence analysis of duplicated actin genes in Lagenidium giganteum and Pythium
A;Reference number: S49007; MUID:94343543; PMID:8064873
A;Accession: S49007
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-365 <BHA>
A;Cross-references: EMBL:X76725
A;Experimental source: strain P3804
C;Superfamily: actin

Query Match 100.0%; Score 71; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15
| | | | | | | | | | | | | | | | | |
Db 126 IQAVLSLYASGRRTTG 140

RESULT 15
A37431
actin, type 1 - Emiliania huxleyi (fragment)
C;Species: Emiliania huxleyi
C;Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A37431
R;Bhattacharya, D.; Stickel, S.K.; Sogin, M.L.
Mol. Biol. Evol. 10, 689-703, 1993
A;Title: Isolation and molecular phylogenetic analysis of actin-coding regions from Emil
A;Reference number: A37431; MUID:93330051; PMID:7687735
A;Contents: CCMF379
A;Accession: A37431
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-365 <BHA>
A;Cross-references: UNIPROT:Q41205; GB:S64188; NID:9404406; PIDN:AAB27626.1; PID:9404407
A;Note: sequence extracted from NCBI backbone (NCBIN:135711, NCBIP:135712)
C;Superfamily: actin

Query Match 100.0%; Score 71; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IQAVLSLYASGRRTTG 15
| | | | | | | | | | | | | | | | | |
Db 126 IQAVLSLYASGRRTTG 140

Search completed: April 8, 2005, 10:53:07
Job time : 10.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351c-10
Perfect score: 71
Sequence: 1 IQAVLSLYASGRRTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	54	2 Q967H7	Q967H7 crassostrea
2	71	100.0	58	2 Q28242	Q28242 cervus elap
3	71	100.0	60	2 Q818B1	Q818b1 tubifex tub
4	71	100.0	60	2 Q818B2	Q818b2 tubifex tub
5	71	100.0	60	2 Q818B3	Q818b3 lumbriculus
6	71	100.0	60	2 Q818B4	Q818b4 limnodrilus
7	71	100.0	60	2 Q818B5	Q818b5 chrysaora c
8	71	100.0	60	2 Q818B7	Q818b7 trichoplax
9	71	100.0	60	2 Q818B9	Q818b9 kudoa ovivo
10	71	100.0	60	2 Q818C0	Q818c0 theloanel
11	71	100.0	60	2 Q818C1	Q818c1 myxobolus p
12	71	100.0	60	2 Q818C2	Q818c2 myxobolus e
13	71	100.0	60	2 Q818C3	Q818c3 myxobolus e
14	71	100.0	60	2 Q818C4	Q818c4 myxobolus m
15	71	100.0	60	2 Q818C5	Q818c5 myxobolus s
16	71	100.0	60	2 Q818C6	Q818c6 myxobolus i
17	71	100.0	85	1 ACT_CHERU	Q39596 chenopodium
18	71	100.0	87	2 Q9FUG2	Q9FUG2 lotus corni
19	71	100.0	95	2 Q81SR2	Q81sr2 spodoptera
20	71	100.0	97	2 Q9JLX9	Q9jlx9 rattus norv
21	71	100.0	104	2 Q11210	Q11210 macaca fasc
22	71	100.0	109	2 Q28916	Q28916 macaca fasc
23	71	100.0	109	2 Q84LA4	Q84la4 festuca aru
24	71	100.0	117	2 Q876P7	Q876p7 elysia chlo
25	71	100.0	117	2 Q800I2	Q800i2 hyla japoni
26	71	100.0	117	2 Q800I3	Q800i3 hyla japoni
27	71	100.0	120	2 Q967I3	Q967i3 thalassios
28	71	100.0	122	2 Q94IA3	Q94ia3 phaseolus v
29	71	100.0	124	2 Q87GW1	Q87gw1 tuber borch
30	71	100.0	124	2 Q9FY43	Q9fy43 trebouxia j
31	71	100.0	125	2 Q802E1	Q802e1 zoarces viv

32 71 100.0 125 2 Q802E2 Q802e2 pachycara b
33 71 100.0 130 2 Q865G0 Q865g0 capra hircu
34 71 100.0 130 2 Q9DE58 Q9de58 coryphaenoi
35 71 100.0 132 2 Q9IA84 Q9ia84 stizostedio
36 71 100.0 133 2 Q9U4L7 Q9u4l7 ageniasepis
37 71 100.0 133 2 Q9U4L8 Q9u4l8 ageniasepis
38 71 100.0 133 2 Q9U4L9 Q9u4l9 ageniasepis
39 71 100.0 133 2 Q9U4M0 Q9u4m0 ageniasepis
40 71 100.0 136 2 Q95V64 Q95v64 ixodes scap
41 71 100.0 142 2 Q9BGH4 Q9bgh4 oryctolagus
42 71 100.0 144 2 Q9OYX9 Q9oyx9 fundulus ne
43 71 100.0 145 2 Q9LL42 Q9ll42 trebouxia j
44 71 100.0 147 2 O04115 O04115 perilla fru
45 71 100.0 147 2 Q7X9B5 Q7x9b5 fragaria an

ALIGNMENTS

RESULT 1

Q967H7 PRELIMINARY; PRT; 54 AA.
ID Q967H7
AC Q967H7
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Actin (Fragment)
OS Crassostrea rhizophorae.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_TaxID=37643;
RN [1]
RP SEQUENCE FROM N.A.
RA Moraes M.O., Rebelo M.F., Junior H.S., Sampaio E.P., Pfeiffer W.C.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY029513; AAK50566.1; -.
DR HSSP; P02568; IMA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
KW Structural protein.
FT NON_TER 1 1
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 5896 MW; 6B12PEA1689A1B9F CRC64;

Query Match 100.0%; Score 71; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15
| | | | | | | | | | | | | | | | | | | | | |
Db 23 IQAVLSLYASGRRTG 37

RESULT 2

Q28242 PRELIMINARY; PRT; 58 AA.
ID Q28242
AC Q28242
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Actin, cytoplasmic 1 (Beta-actin) (Fragment).
GN Name=ACTB;
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.

```

NCBI_TaxID=9860;
[1]
SEQUENCE FROM N.A.
TISSUE=Antler;
MEDLINE=98233260; PubMed=9571767;
DOI=10.1002/(SICI)1097-010X(19980501)281:1<36::AID-JEZ6>3.0.CO;2-D;
Francis S.M., Suttie J.M.;
"Detection of growth factors and proto-oncogene mRNA in the growing
tip of red deer (Cervus elaphus) antler using reverse-transcriptase
polymerase chain reaction (RT-PCR).";
J. Exp. Zool. 281:36-42(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells.
CC -!- SUBUNIT: Polymerization of globular actin (G-actin) leads to a
CC structural filament (F-actin) in the form of a two-stranded helix.
CC Each actin can bind to 4 others.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SUBCELLULAR LOCATION: In vertebrates 3 main groups of actin isoforms,
CC alpha, beta and gamma have been identified. The alpha actins are
CC found in muscle tissues and are a major constituent of the
CC contractile apparatus. The beta and gamma actins co-exist in most
CC cell types as components of the cytoskeleton and as mediators of
CC internal cell motility.
CC -!- SIMILARITY: Belongs to the actin family.
EMBL; U62112; AAB05258.1; -.
HSSP; P02577; 1NM1.
GO; GO:0015629; F:actin cytoskeleton; IEA.
GO; GO:0005200; C:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
PROSITE; PS00406; ACTINS_1; PARTIAL.
PROSITE; PS00432; ACTINS_2; PARTIAL.
PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
Cytoskeleton; Multigene family; Structural protein.
NON_TER 1 1
FT CHAIN <1 >58 ACTIN, CYTOPLASMIC 1.
NON_TER 58 58
SEQUENCE 58 AA; 6250 MW; 26D0DBBCE629A61 CRC64;

Query Match 100.0%; Score 71; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRITG 15
DB 17 IQAVLSLYASGRITG 31
|||||
|||||

RESULT 3
Q818B1 PRELIMINARY; PRT; 60 AA.
ID Q818B1
AC Q818B1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (fragment).
OS Tubifex tubifex (Sludge worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Tubificina; Tubificidae; Tubifex.
OC NCBI_TaxID=6386;
OX NCBI_TaxID=9860;
[1]
SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
RL -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
EMBL; AY157023; AAN85108.1; -.
HSSP; P02568; 1MA9.
GO; GO:0015629; C:actin cytoskeleton; IEA.

```

```

(1)
RN SEQUENCE FROM N.A.
RP Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AV157021; AAN85106.1; -.
DR HSSP; P02568; 1MA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6500 MW; 77C6CFABD3D424AC CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
Db |||||
36 IQAVLSLYASGRRTTG 50

RESULT 6
Q818B4 PRELIMINARY; PRT; 60 AA.
AC Q818B4;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Limodrilus hoffmeisteri.
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Tubificina; Tubificidae; Limodrilus.
OX NCBI_TaxID=76587;
RN (1)
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AV157020; AAN85105.1; -.
DR HSSP; P02568; 1MA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6500 MW; 77C6CFABD3D424AC CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
Db |||||
36 IQAVLSLYASGRRTTG 50

RESULT 7
Q818B5 PRELIMINARY; PRT; 60 AA.
AC Q818B5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Chrysaora colorata (purpl-striped jelly).
OC Eukaryota; Metazoa; Cnidaria; Scyphozoa; Semeostomeae; Pelagiidae;
OC Chrysaora.
OX NCBI_TaxID=168767;
RN (1)
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157019; AAN85104.1; -.
DR HSSP; P02568; 1MA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6492 MW; 22733BABD3D32866 CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
Db |||||
36 IQAVLSLYASGRRTTG 50

RESULT 8
Q818B7 PRELIMINARY; PRT; 60 AA.
AC Q818B7;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Trichoplax adhaerens.
OC Eukaryota; Metazoa; Placozoa; Trichoplax.
OX NCBI_TaxID=10228;
RN (1)
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157017; AAN85102.1; -.
DR HSSP; P02568; 1MA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6542 MW; CC8C249808B854A6 CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
Db |||||
36 IQAVLSLYASGRRTTG 50
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Fri Apr 8 14:14:16 2005

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QY 1 IQAVLSLYASGRRTG 15
DB 36 IQAVLSLYASGRRTG 50

RESULT 9
Q818B9 PRELIMINARY; PRT; 60 AA.
AC Q818B9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative beta-actin (Fragment).
OS Kudoa ovivora
OC Eukaryota; Metazoa; Myxozoa; Myxosporea; Multivalvulida; Kudoidea;
OC Kudoa.
OX NCBI_TaxID=210917;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157015; AAN85100.1; -.
DR HSSP; P02568; 1MA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
FT SEQUENCE 60 AA; 6496 MW; 8DDC75A1D3D435A1 CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
DB 36 IQAVLSLYASGRRTG 50

RESULT 10
Q818C0 PRELIMINARY; PRT; 60 AA.
AC Q818C0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative beta-actin (Fragment).
OS Thelehanellus nikolskii.
OC Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysoptorina;
OC Myxobolidae; Thelehanellus.
OX NCBI_TaxID=215725;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157014; AAN85099.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.

QY 1 IQAVLSLYASGRRTG 15
DB 36 IQAVLSLYASGRRTG 50

RESULT 11
Q818C1 PRELIMINARY; PRT; 60 AA.
AC Q818C1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative beta-actin (Fragment).
OS Myxobolus pavlovskii.
OC Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysoptorina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=195467;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157013; AAN85098.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
FT SEQUENCE 60 AA; 6486 MW; 7D7DC5A1D3D424B1 CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
DB 36 IQAVLSLYASGRRTG 50

RESULT 12
Q818C2 PRELIMINARY; PRT; 60 AA.
AC Q818C2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative beta-actin (Fragment).
OS Myxobolus episcuamalis.
OC Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysoptorina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=204748;
RN [1]
RP SEQUENCE FROM N.A.

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```
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157012; AAN85097.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6484 MW; 3D93D5A1D3D424A7 CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
Db 36 IQAVLSLYASGRRTG 50

RESULT 13
Q818C3
ID Q818C3 PRELIMINARY; PRT; 60 AA.
AC Q818C3;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus exiguus.
OC Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysporina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=204750;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157011; AAN85096.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6532 MW; C383DFABD3D424AA CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
Db 36 IQAVLSLYASGRRTG 50

RESULT 14
Q818C4
ID Q818C4 PRELIMINARY; PRT; 60 AA.
AC Q818C4;
```

```
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus muelleri.
OC Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysporina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=204749;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157010; AAN85095.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6498 MW; 3983D5A1D3D424A7 CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
Db 36 IQAVLSLYASGRRTG 50

RESULT 15
Q818C5
ID Q818C5 PRELIMINARY; PRT; 60 AA.
AC Q818C5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus spinacurvatura.
OC Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysporina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=182349;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157009; AAN85094.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6498 MW; 3983D5A1D3D424A7 CRC64;

Query Match 100.0%; Score 71; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
Db 36 IQAVLSLYASGRRTG 50
```

us-09-423-351c-10.rup

Fri Apr 8 14:14:16 2005

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IQAVLSLYASGRITG 15
Db 36 IQAVLSLYASGRITG 50

Search completed: April 8, 2005, 12:03:13
Job time : 58.8667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351c-11

Perfect score: 75

Sequence: 1 KILTERGYSTTTAE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	15	2 AAW92537	Beta-acti
2	75	100.0	15	4 AAB45794	Human aut
3	75	100.0	97	4 AAM13687	Peptide #
4	75	100.0	97	4 ABR32618	Peptide #
5	75	100.0	97	4 AAM26087	Peptide #
6	75	100.0	97	4 ABE27467	Human pep
7	75	100.0	97	4 ABB18116	Protein #
8	75	100.0	97	4 AAM65825	Human bon
9	75	100.0	97	4 AAM53448	Human bra
10	75	100.0	97	4 AEG47471	Human liv
11	75	100.0	97	4 AAM01437	Peptide #
12	75	100.0	97	5 ABG35459	Human pep
13	75	100.0	148	5 ADK36534	Novel hum
14	75	100.0	153	4 ABG15497	Novel hum
15	75	100.0	164	3 ABG37312	Arabidops
16	75	100.0	168	5 ABP42912	Human ova
17	75	100.0	186	3 AAG38701	Arabidops
18	75	100.0	186	3 AAG47774	Arabidops
19	75	100.0	196	6 ABU70816	Human adi
20	75	100.0	229	3 AAG38700	Arabidops
21	75	100.0	246	3 AAG38699	Arabidops
22	75	100.0	274	6 ABU70549	Human adi
23	75	100.0	276	3 AAG50947	Arabidops
24	75	100.0	277	3 AAG05115	Arabidops
25	75	100.0	294	7 ADI63068	Human apo

26	75	100.0	304	3 AAG50946	Arabidops
27	75	100.0	305	3 AAG05114	Arabidops
28	75	100.0	321	3 AAG50945	Arabidops
29	75	100.0	322	3 AAG05113	Arabidops
30	75	100.0	332	3 AAG50873	Arabidops
31	75	100.0	332	3 AAG37317	Arabidops
32	75	100.0	332	3 AAG44697	Zeae maye
33	75	100.0	332	3 AAG24178	Arabidops
34	75	100.0	332	3 AAG05583	Arabidops
35	75	100.0	332	3 AAG47761	Arabidops
36	75	100.0	332	3 AAG50944	Arabidops
37	75	100.0	332	3 AAG34599	Arabidops
38	75	100.0	332	3 AAG54243	Arabidops
39	75	100.0	332	3 AAG47770	Arabidops
40	75	100.0	332	7 ADI63011	Human apo
41	75	100.0	345	3 AAG47748	Arabidops
42	75	100.0	360	3 AAG47760	Arabidops
43	75	100.0	360	3 AAG47769	Arabidops
44	75	100.0	360	3 AAG50872	Arabidops
45	75	100.0	360	3 AAG05582	Arabidops

ALIGNMENTS

RESULT 1

AAW92537
ID AAW92537 standard; peptide; 15 AA.

XX AC AAW92537;

DT 26-APR-1999 (first entry)

DE Beta-actin reference peptide substrate #11.

KW Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
KW binding agent; substrate-binding site; SBS; substrate folding; actin;
KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
KW reduced toxicity.

XX OS Synthetic.

XX WO9853322-A1.

PD 26-NOV-1998.

PF 22-MAY-1998; 98WO-GB001485.

PR 23-MAY-1997; 97GB-00010762.

PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

PI Willison K, Hynes G, Liou AK;

WPI; 1999-070162/06.

PT Identifying specific binding agents for substrate binding site in CCT
PT chaperonin complex also new peptide binding agents and their mimetics,
PT and peptides containing a specific CCT binding site, used for treating
cancer.

PS Disclosure; Fig 10; 97pp; English.

CC This invention describes a method which uses the CCT (eukaryotic type II
CC chaperonin) complex or part of it, for identifying a binding agent that
CC can occupy a substrate-binding site (SBS) on the CCT complex. By binding
CC to the CCT complex, the binding agents block an SBS so that biological
CC activity of the CCT complex is affected, particularly its ability to fold
CC substrates such as actin, tubulin and cyclin. The binding agents are
CC useful for treatment of cancer, particularly when used in combination
CC with an anticancer drug, or viral infections. Nucleic acid fragments are
CC used to screen for agents, e.g. binding agents that modulate interaction
CC between the CCT complex and a protein that is to be folded. The binding

5

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RESULT 4
ABB32618
ID ABB32618 standard; peptide; 97 AA.
XX
AC ABB32618;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #124 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 25253; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 97 AA;
XX
Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTTAE 15
DB 70 KILTERGYSFTTTAE 84

RESULT 5
AAM26087
ID AAM26087 standard; protein; 97 AA.
XX
AC AAM26087;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #124 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
OS Homo sapiens.

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XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 26356; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP;
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 97 AA;
XX
Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTTAE 15
DB 70 KILTERGYSFTTTAE 84

RESULT 6
ABB27467
ID ABB27467 standard; peptide; 97 AA.
XX
AC ABB27467;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human peptide #118 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast; disease;
XX cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000662.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

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Fri Apr 8 14:14:16 2005

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-48899/53.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts.
 XX
 XX Claim 15; SEQ ID NO 19886; 530pp; English.
 XX
 XX The present invention relates to single exon nucleic acid probes for
 XX measuring human gene expression in a sample derived from human heart (see
 XX AB21535-ABA41305). The present sequence is a protein encoded by one such
 XX probe. The probes may be used for predicting, measuring and displaying
 XX gene expression in samples derived from the human heart via microarrays.
 XX By measuring gene expression, the probes are useful for predicting,
 XX diagnosing, grading, staging, monitoring and prognosing diseases of the
 XX human heart and vascular system e.g. cardiovascular disease,
 XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 XX sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 97 AA;
 XX
 XX Query Match 100.0%; Score 75; DB 4; Length 97;
 XX Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KILTERGYSTTTAAE 15
 Db |||||
 70 KILTERGYSTTTAAE 84
 RESULT 8
 AAM65825
 ID AAM65825 standard; protein; 97 AA.
 XX AC AAM65825;
 XX
 XX 06-NOV-2001 (first entry)
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26131.
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 XX microarray; cancer; leukaemia; lymphoma; myeloma.
 XX Homo sapiens.
 XX WO200157276-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000668.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-48899/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human bone marrow.
 XX Example 4; SEQ ID NO 26131; 658pp + Sequence Listing; English.
 PS

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-496933/54.
 XX
 XX New spatially-addressable set of single exon nucleic acid probes, useful
 XX for measuring gene expression in sample derived from human breast,
 XX comprises number of single exon nucleic acid probes.
 XX
 XX Claim 27; SEQ ID NO 10435; 327pp + Sequence Listing; English.
 XX
 XX The invention relates to a spatially-addressable set of single exon
 XX nucleic acid probes for measuring gene expression in a sample derived
 XX from human breast and Bt 474 cells. The method involves contacting the
 XX probes with a collection of detectably labelled nucleic acids derived
 XX from mRNA of human breast, and then measuring the label bound to each
 XX probe of the microarray. The probes are useful for verifying the
 XX expression of regions of genomic DNA predicted to encode proteins. They
 XX are useful for gene discovery, and for determining predisposition and/or
 XX prognosing breast disease. Gene expression analysis is useful for
 XX assessing the toxicity of chemical agents on cells. The microarray of
 XX this invention presents a far greater diversity of probes for measuring
 XX gene expression, with far less bias than expressed sequence tag
 XX microarrays. The method is suitable for rapid production of functional
 XX information from genomic sequence. The present sequence is a peptide
 XX encoded by a single exon nucleic acid probe of the invention. Note: The
 XX sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 97 AA;
 XX
 XX Query Match 100.0%; Score 75; DB 4; Length 97;
 XX Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KILTERGYSTTTAAE 15
 Db |||||
 70 KILTERGYSTTTAAE 84
 RESULT 7
 ABB18116
 ID ABB18116 standard; protein; 97 AA.
 XX AC ABB18116;
 XX
 XX 23-JAN-2002 (first entry)
 XX Protein #115 encoded by probe for measuring heart cell gene expression.
 XX Human; gene expression; heart; microarray; vascular system;
 XX cardiovascular disease; hypertension; cardiac arrhythmia;
 XX congenital heart disease.
 XX Homo sapiens.
 XX WO200157274-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000666.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA

XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX
 SQ Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSTTTAE 15
 DB 70 KILTERGYSTTTAE 84

RESULT 9
 AAM53448
 ID AAM53448 standard; protein; 97 AA.

XX
 AC AAM53448;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25553.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 KW
 XX Homo sapiens.

OS
 XX WO200157275-A2.

PN
 XX 09-AUG-2001.

PD
 XX 30-JAN-2001; 2001WO-US000667.

PF
 XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human
 CC brains.
 CC Example 4; SEQ ID NO 25553; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, of
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention

XX
 SQ Sequence 97 AA;
 Query Match 100.0%; Score 75; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSTTTAE 15
 DB 70 KILTERGYSTTTAE 84

RESULT 10
 ABG47471

ID ABG47471 standard; peptide; 97 AA.

XX
 AC ABG47471;

DT 25-FEB-2003 (first entry)

DE Human liver peptide, SEQ ID NO 26119.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 KW
 XX Homo sapiens.

OS
 XX WO200157273-A2.

PN
 XX 09-AUG-2001.

PD
 XX 30-JAN-2001; 2001WO-US000664.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 CC gene expression in human adult liver.
 CC Claim 27; SEQ ID NO 26119; 650pp; English.
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG5930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 97 AA;

XX Query Match 100.0%; Score 75; DB 4; Length 97;
 XX Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSTTTAE 15
 DB 70 KILTERGYSTTTAE 84

RESULT 11
 AAM01437

Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesia; pulmonary hypertension; hyaline membrane disease.

Homo sapiens.

WO200186003-A2.

15-NOV-2001.

30-JAN-2001; 2001WO-US000665.

04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Claim 27; SEQ ID NO 25124; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon of microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types comprising one of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAE 15
|||||
DB 70 KILTERGYSFTTAE 84

RESULT 13
ADK36534
ID ADK36534 standard; protein; 148 AA.

XX AC ADK36534;

XX DT 06-MAY-2004 (first entry)

XX DE Novel human polypeptide SeqID8616.

XX KW antiarthritic; antiparkinsonian; neuroprotective; nootropic;
KW immunosuppressive; cytostatic; antipsoriatic; antiinflammatory;
KW antibacterial; antiviral; antifungal; antiparasitic; gene therapy;
KW arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer;
KW psoriasis; inflammatory bowel disease; infection; bacteria; virus;
KW fungus; parasite; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 1..148

FT /label= OTHER

FT /note= "OTHER= All Xaa's in this sequence are unknown
FT amino acids or the site of a stop codon within the DNA
FT sequence"

XX PN WO200216439-A2.

XX PD 28-FEB-2002.

XX PF 05-MAR-2001; 2001WO-US004941.

XX PR 07-MAR-2000; 2000US-00519705.

XX PR 19-MAY-2000; 2000US-00574454.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2002-280918/32.

XX PT Isolated polynucleotide encoding bone marrow derived polypeptides useful
XX for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
XX disease, and inflammatory bowel disease.

XX PS Claim 20; SEQ ID NO 8616; 504pp; English.

XX CC This invention relates to a novel isolated polynucleotide comprising a
XX nucleotide sequence selected from one of 1680 sequences, a mature protein
XX coding portion of them, an active domain of them and their complementary
XX sequences. The invention may be useful for the production of compounds
XX with an antiarthritic, antiparkinsonian, neuroprotective, nootropic,
XX immunosuppressive, cytostatic, antipsoriatic, antiinflammatory,
XX antibacterial, antiviral, antifungal or antiparasitic activity. In
XX addition, the disclosed sequences may be useful for gene therapy. The
XX polypeptides or their antibodies are useful for treating many diseases
XX such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,
XX psoriasis, inflammatory bowel disease and infections caused by bacteria,
XX viruses, fungi or parasites. The present sequence is that of a human

CC polypeptide of the invention.

XX SQ Sequence 148 AA;

Query Match 100.0%; Score 75; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSFTTAE 15
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DB 50 KILTERGYSFTTAE 64

RESULT 14

ABG15497

ID ABG15497 standard; protein; 153 AA.

XX AC ABG15497;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #15488.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX N-PSDB; AAS79684.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.

XX PS Claim 20; SEQ ID NO 45856; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG030377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

Fri Apr 8 14:14:16 2005

us-09-423-351c-11.rag

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SQ Sequence 153 AA;
Query Match 100.0%; Score 75; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILTERGYSTTTAE 15
   |||||
Db 32 KILTERGYSTTTAE 46

RESULT 15
AAG37312
ID AAG37312 standard; protein; 164 AA.
XX
AC AAG37312;
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45859.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0121180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
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PR 09-AUG-1999; 99US-0147493P.
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Best Local Similarity 100.0%; Pred. No. 5e-05;
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SUMMARIES

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4	75	100.0	375	4	US-09-976-594-731
5	75	100.0	399	4	US-09-949-016-9424
6	75	100.0	404	4	US-09-949-016-11313
7	70	93.3	239	3	US-09-949-016-10409
8	70	93.3	375	3	US-09-106-217-16
9	70	93.3	376	1	US-08-588-113-2
10	70	93.3	376	4	US-09-949-016-6100
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12	70	93.3	377	4	US-09-919-172-33
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19	63	84.0	375	4	US-09-631-022-7
20	63	84.0	375	4	US-09-631-022-8
21	60	80.0	371	1	US-08-261-206A-77
22	59	78.7	375	2	US-08-494-151-14
23	47	62.7	10	4	US-09-786-066-11
24	41	54.7	368	4	US-09-489-039A-9556
25	40	53.3	97	4	US-09-489-039A-10490
26	40	53.3	97	4	US-09-489-039A-13415
27	40	53.3	116	4	US-09-248-796A-17470

ALIGNMENTS

RESULT 1

US-09-306-446C-5
; Sequence 5, Application US/09306446C

; Patent No. 6372959

; GENERAL INFORMATION:

; APPLICANT: KIM, Dong Soo

; APPLICANT: KIM, Chul Geun

; APPLICANT: NAM, Yoon Kwon

; APPLICANT: NOH, Jae Koo

; APPLICANT: CHO, Kyou Nam

; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE

; FILE REFERENCE: P06344US0/BAS

; CURRENT APPLICATION NUMBER: US/09/306,446C

; CURRENT FILING DATE: 1999-05-06

; PRIOR APPLICATION NUMBER: KR 98/20255

; PRIOR FILING DATE: 1998-06-01

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 5

; LENGTH: 146

; TYPE: PRT

; ORGANISM: Misgurnus mizolepus

US-09-306-446C-5

Query Match 100.0%; Score 75; DB 3; Length 146;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAE 15

Db 70 KILTERGYSFTTAE 84

RESULT 2

US-08-609-236-6

; Sequence 6, Application US/08609236

; Patent No. 6087398

; GENERAL INFORMATION:

; APPLICANT: Steven R. Goodman

; TITLE OF INVENTION: No. 6087398el Sickie Cell Anemia Treatment

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McGregor & Adler, LLP

; STREET: 8011 Candle Lane

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,236
FILING DATE: March 1, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 374
TYPE: Amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:

US-08-609-236-6

Query Match 100.0%; Score 75; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
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Db 190 KILTERGYSFTTAAE 204
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RESULT 3

US-09-306-446C-2
Sequence 2, Application US/09306446C
Patent No. 6372959
GENERAL INFORMATION:
APPLICANT: KIM, Dong Soo
APPLICANT: KIM, Chul Geun
APPLICANT: NAM, Yoon Kwon
APPLICANT: NOH, Jae Koo
APPLICANT: CHO, Kyou Nam
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
FILE REFERENCE: P06344US0/BAS
CURRENT APPLICATION NUMBER: US/09/306,446C
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: KR 98/20255
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 374
TYPE: PRT
ORGANISM: Misgurnus mizolepus

Query Match 100.0%; Score 75; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KILTERGYSFTTAAE 15
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Db 191 KILTERGYSFTTAAE 205
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RESULT 4

US-09-976-594-731
Sequence 731, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match 100.0%; Score 75; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
|||||

Db 191 KILTERGYSFTTAAE 205
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RESULT 5

US-09-949-016-9424
Sequence 9424, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9424
LENGTH: 399
TYPE: PRT
ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 75; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
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Db 215 KILTERGYSFTTAAE 229
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RESULT 6
US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match 100.0%; Score 75; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFVTTAE 15
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Db 220 KILTERGYSFVTTAE 234

RESULT 7
US-09-949-016-10409
; Sequence 10409, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10409
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10409

Query Match 93.3%; Score 70; DB 4; Length 239;
Best Local Similarity 93.3%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KILTERGYSFVTTAE 15
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Db 55 KILTERGYSFVTTAE 69

RESULT 8
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
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; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-16

Query Match 93.3%; Score 70; DB 3; Length 375;
Best Local Similarity 93.3%; Pred. No. 0.00033;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KILTERGYSFVTTAE 15
|||||
Db 191 KILTERGYSFVTTAE 205

RESULT 9
US-08-588-113-2
; Sequence 2, Application US/08588113
; Patent No. 5710003
; GENERAL INFORMATION:
; APPLICANT: McHugh, Kirk M.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5710003ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,113
; FILING DATE:
; CLASSIFICATION: 436
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; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: TLU-1652
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-588-113-2

Query Match 93.3%; Score 70; DB 1; Length 376;
Best Local Similarity 93.3%; Pred. No. 0.00033;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KILTERGYSFVTTAE 15
Db 192 KILTERGYSFVTTAE 206

RESULT 10
US-09-949-016-6100
; Sequence 6100, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6100
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6100

Query Match 93.3%; Score 70; DB 4; Length 376;
Best Local Similarity 93.3%; Pred. No. 0.00033;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KILTERGYSFVTTAE 15
Db 192 KILTERGYSFVTTAE 206

RESULT 11
US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rochwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington

; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patcin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-2

Query Match 93.3%; Score 70; DB 3; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00033;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KILTERGYSFVTTAE 15
Db 193 KILTERGYSFVTTAE 207

RESULT 12
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match 93.3%; Score 70; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00033;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KILTERGYSFVTTAE 15
Db 193 KILTERGYSFVTTAE 207

RESULT 13
US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204

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; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0601/7224 (JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 93.3%; Score 70; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00033;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KILTERGYSFVTTAE 15
Db 193 KILTERGYSFVTTAE 207

RESULT 14
US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

Query Match 93.3%; Score 70; DB 4; Length 386;
Best Local Similarity 93.3%; Pred. No. 0.00034;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KILTERGYSFVTTAE 15
Db 202 KILTERGYSFVTTAE 216

RESULT 15
US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match 93.3%; Score 70; DB 4; Length 402;
Best Local Similarity 93.3%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KILTERGYSFVTTAE 15
Db 218 KILTERGYSFVTTAE 232

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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	75	100.0	97	US-09-864-761-33414	Sequence 33414, A
2	75	100.0	168	US-10-264-049-4044	Sequence 4044, Ap
3	75	100.0	179	US-10-437-963-203848	Sequence 203848
4	75	100.0	180	US-10-437-963-169247	Sequence 169247, A
5	75	100.0	230	US-10-767-701-42770	Sequence 42770, A
6	75	100.0	236	US-10-424-599-206389	Sequence 206389
7	75	100.0	237	US-10-424-599-143226	Sequence 143226
8	75	100.0	238	US-10-437-963-162706	Sequence 162706
9	75	100.0	249	US-10-767-701-43575	Sequence 43575, A
10	75	100.0	261	US-10-424-599-177530	Sequence 177530
11	75	100.0	288	US-10-425-114-57500	Sequence 57500, A
12	75	100.0	331	US-10-425-114-59172	Sequence 59172, A
13	75	100.0	371	US-10-322-281-68	Sequence 68, Appl

14	75	100.0	375	14	US-10-205-194-93	Sequence 93, Appl
15	75	100.0	375	14	US-10-316-253-88	Sequence 88, Appl
16	75	100.0	375	15	US-10-205-331-94	Sequence 94, Appl
17	75	100.0	375	15	US-10-260-708-82	Sequence 82, Appl
18	75	100.0	376	16	US-10-437-963-202420	Sequence 202420
19	75	100.0	377	15	US-10-424-599-222816	Sequence 222816
20	75	100.0	377	15	US-10-424-599-223492	Sequence 223492
21	75	100.0	377	15	US-10-425-114-66124	Sequence 66124, A
22	75	100.0	378	15	US-10-425-114-52458	Sequence 52458, A
23	75	100.0	378	15	US-10-425-114-59265	Sequence 59265, A
24	75	100.0	378	15	US-10-425-114-59967	Sequence 59967, A
25	75	100.0	378	15	US-10-425-114-61003	Sequence 61003, A
26	75	100.0	380	16	US-10-437-963-106736	Sequence 106736
27	75	100.0	380	16	US-10-437-963-187415	Sequence 187415
28	75	100.0	383	16	US-10-767-701-47319	Sequence 47319, A
29	75	100.0	391	16	US-10-437-963-130713	Sequence 130713
30	75	100.0	398	16	US-10-322-281-63	Sequence 63, Appl
31	75	100.0	413	9	US-09-925-301-1436	Sequence 1436, Ap
32	75	100.0	421	16	US-10-437-963-186750	Sequence 186750
33	72	96.0	375	15	US-10-369-493-5927	Sequence 5927, Ap
34	71	94.7	254	15	US-10-425-114-69353	Sequence 69353, A
35	71	94.7	299	15	US-10-424-599-278431	Sequence 278431
36	71	94.7	377	15	US-10-424-599-162009	Sequence 162009
37	71	94.7	377	16	US-10-437-963-121952	Sequence 121952
38	71	94.7	377	16	US-10-437-963-148877	Sequence 148877
39	71	94.7	377	16	US-10-437-963-198295	Sequence 198295
40	71	94.7	377	16	US-10-767-701-47239	Sequence 47239, A
41	71	94.7	379	15	US-10-424-599-278432	Sequence 278432
42	71	94.7	381	15	US-10-424-599-280814	Sequence 280814
43	71	94.7	384	15	US-10-425-114-44853	Sequence 44853, A
44	71	94.7	393	15	US-10-425-114-58706	Sequence 58706, A
45	71	94.7	393	15	US-10-425-114-65854	Sequence 65854, A

ALIGNMENTS

RESULT 1
US-09-864-761-33414
; Sequence 33414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

Db 126 KILTERGYSFTTTAE 140

RESULT 5

US-10-767-701-42770
; Sequence 42770, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42770
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17410_1.pep
US-10-767-701-42770

Query Match 100.0%; Score 75; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTTAE 15
|||||
Db 193 KILTERGYSFTTTAE 207

RESULT 6

US-10-424-599-206389
; Sequence 206389, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206389
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(236)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28396C.1.pep
US-10-424-599-206389

Query Match 100.0%; Score 75; DB 15; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTTAE 15
|||||
Db 61 KILTERGYSFTTTAE 75

RESULT 7

US-10-424-599-143226
; Sequence 143226, Application US/10424599

; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143226
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(237)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100347C.1.pep
US-10-424-599-143226

Query Match 100.0%; Score 75; DB 15; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTTAE 15
|||||
Db 75 KILTERGYSFTTTAE 89

RESULT 8

US-10-437-963-162706
; Sequence 162706, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162706
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(238)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61772C.1.pep
US-10-437-963-162706

Query Match 100.0%; Score 75; DB 16; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTTAE 15
|||||
Db 44 KILTERGYSFTTTAE 59

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RESULT 9
US-10-767-701-43575
; Sequence 43575, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 43575
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5949_1.pep
US-10-767-701-43575

Query Match 100.0%; Score 75; DB 16; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
| | | | | | | | | | | | | | |
Db 65 KILTERGYSFTTAAE 79

RESULT 10
US-10-424-599-177530
; Sequence 177530, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177530
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131325C.1.pep
US-10-424-599-177530

Query Match 100.0%; Score 75; DB 15; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
| | | | | | | | | | | | | | |
Db 77 KILTERGYSFTTAAE 91

RESULT 11
US-10-425-114-57500
; Sequence 57500, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57500
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROB73004G09_FLI.pep
US-10-425-114-57500

Query Match 100.0%; Score 75; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
| | | | | | | | | | | | | | |
Db 104 KILTERGYSFTTAAE 118

RESULT 12
US-10-425-114-59172
; Sequence 59172, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59172
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700332871_FLI.pep
US-10-425-114-59172

Query Match 100.0%; Score 75; DB 15; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
| | | | | | | | | | | | | | |
Db 147 KILTERGYSFTTAAE 161

RESULT 13
US-10-322-281-68
; Sequence 68, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371
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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57500
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROB73004G09_FLI.pep
US-10-425-114-57500

Query Match 100.0%; Score 75; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
| | | | | | | | | | | | | | |
Db 104 KILTERGYSFTTAAE 118

RESULT 12
US-10-425-114-59172
; Sequence 59172, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59172
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700332871_FLI.pep
US-10-425-114-59172

Query Match 100.0%; Score 75; DB 15; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILTERGYSFTTAAE 15
| | | | | | | | | | | | | | |
Db 147 KILTERGYSFTTAAE 161

RESULT 13
US-10-322-281-68
; Sequence 68, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371
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